

Table 8

5318	db mining	Hs.75969	AI568695	4532069	proline-rich protein with nuclear targeting signal (B4-2), mRNA /cds=(113,1096)	-1	AAAACCATTCCAGCTTAATGCCTTAA TTTTAATGCCAACAAAATGGGG
5319	Table 3A	NA	AI568725	4532099	th15a01.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2118312 3', mRNA sequence	-1	TGCAACCTCTTAAATGTGGGCTAC TGGAGATCATGCCACTGCACTCCA
5320	Table 3A	Hs.159014	AI568751	4532125	th15d09.x1 cDNA, 3' end /clone=IMAGE:2118353 /clone_end=3'	-1	AGCTCAGATGGTCCCCAAAAGAGG CATAGGAAAGCGCGACCTCACTGCC
5321	db mining	Hs.174242	AI568753	4532127	th15e04.x1 cDNA, 3' end /clone=IMAGE:2118366 /clone_end=3'	-1	CAAATAAAAAGGCTGGGCAAAGG TGGGCACCAAAAGTCCTCTATGTG
5322	Table 3A	NA	AI568755	4532129	th15f03.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2118365 3', mRNA sequence	-1	TGCAGCTCCCATTCTGAGCGTCTA CCAGGTACTAGGAGAACTCTTACA
5323	db mining	Hs.327876	AI568771	4532145	th15h04.x1 cDNA, 3' end /clone=IMAGE:2118391 /clone_end=3'	-1	ATTATCCTTTCCCCAGGAAGCCCTC GCCCCCCAAAAGGGAACAGTTT
5324	db mining	Hs.179070	AI568773	4532147	th15h09.x1 cDNA, 3' end /clone=IMAGE:2118401 /clone_end=3'	-1	CATGAGCCCAGGGTTTCATGACAAA CATTACTAGCATGTTCAACTGCC
5325	Table 3A	NA	AI569898	4533272	tr57c12.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2222422 3' similar to gb:D16234 PROBABLE PROTEIN DISULFID	-1	GCCCGGTTATGGAAAACCAGGAC CAGTTATGTTGGGTTTGGGAA
5326	Table 3A	Hs.92448	AI570295	4533669	EST390664 cDNA	-1	GCTTGGTACTGTCATAGTGATTACAA ATTTCATGGAATGCGAAGCAC
5327	Table 3A	Hs.5637	AI570531	4533905	602998983F1 cDNA, 5' end /clone=IMAGE:5141013 /clone_end=5'	-1	TTTCTCCCTCTCTTCCCCTTCCAC GAACTGCAATACCAAGTAACCTTGG
5328	Table 3A	Hs.14623	AI571519	4534893	interferon, gamma-inducible protein 30 (IFI30), mRNA /cds=(40,951)	-1	AAGCCCAGATAACAAAATTCCACCC CATGATCAAGAACCTGCTCCACT
5329	db mining	Hs.8882	AI572757	4536131	tu43c07.x1 cDNA, 3' end /clone=IMAGE:2253804 /clone_end=3'	-1	CATGTGTTGACTCTGTAATGGATTAT GTAGCCCCACTTCAGTCTGCAAAT
5330	Table 3A	Hs.230430	AI579979	4564355	tq45a01.x1 cDNA, 3' end /clone=IMAGE:2211720 /clone_end=3'	-1	AGGGGTGCCCCTTTCCCCTCATGT AAAATTCTAACTGGGGCTACCAGT
5331	Table 3A	NA	AI581199	4565575	tl94h10.x1 NCI_CGAP_Co14 cDNA clone IMAGE:2154787 3' similar to SWATP6_HUMAN P00846 ATP SYNTHASE A	-1	TCTACTGACTATCCTAGAAATCGCTG TCGCCCTTAATCCAAGCCTACGTTT
5332	Table 3A	Hs.327922	AI581383	4565759	to1c02.x1 cDNA, 3' end /clone=IMAGE:2183714 /clone_end=3'	-1	TGAAGAAAATGCCCTTCTGTGATGT TTTGAATACTACCCAACAGCCAA
5333	Table 3A	Hs.229918	AI581732	4567629	ar74f03.x1 cDNA, 3' end /clone=IMAGE:2128349 /clone_end=3'	-1	CTTCCTAGGCCCTAAGTTGGCCTTTG GGTGGCTCCAAAAGGATTAGGTT
5334	Table 3A	Hs.292553	AI582954	4568851	tr98e07.x1 cDNA, 3' end /clone=IMAGE:2227140 /clone_end=3'	-1	TCCCCCTCGTTTGTAGGGTTGTAC ATAATAAAACAATGGGGGGGGCC
5335	Table 3A	Hs.340925	AI590337	4599385	wh96a06.x1 cDNA, 3' end /clone=IMAGE:2388562 /clone_end=3'	-1	TGTTAAAGTGTGAGGTTTCTGAACCC TTAGCAGAAGGACTTTAATGTTT
5336	Table 3A	Hs.101617	AI597917	4605976	601513709F1 cDNA, 5' end /clone=IMAGE:3914786 /clone_end=5'	-1	AGTTCCACTGCTTCCCTTACCTT GATTAATGCCATATGCTACTT
5337	db mining	Hs.13646	AI611245	4620412	601287348F1 cDNA, 5' end /clone=IMAGE:3621754 /clone_end=5'	-1	AGTTCTGTTGTGTAATCTGGGCTGG TCCCCTGGGATATGTATTCTGTG
5338	Table 3A	NA	AI619574	4628700	ty50c09.x1 NCI_CGAP_Ut2 cDNA clone IMAGE:2282512 3' similar to gb:M23813 NUCLEOLAR PHOSPHOPROTEIN B	-1	CCCCCTTGCTTGGTTAAAGTAGGTA TGGAAATGTTATTATAGGCCATAGT
5339	db mining	Hs.340584	AI625119	4650050	ts47b12.x1 cDNA, 3' end /clone=IMAGE:2231711 /clone_end=3'	-1	TCAGTGAAACATAATTAGGCCGTGA GTTTTTGCTCTACTCCCAAGGTTT
5340	Table 3A	Hs.188365	AI625368	4650299	ts37c10.x1 cDNA, 3' end /clone=IMAGE:2230770 /clone_end=3'	-1	TGTAAACTTGTAAACAACTTTTC AACATTTGGCCGGGGTATTCCC
5341	Table 3A	Hs.278554	AI627495	4664295	chromobox homolog 3 (Drosophila HP1 gamma) (CBX3), mRNA /cds=(111,662)	-1	TGCTGAAAGTGGTCCCCAAAAGGGTA CTAGTTTTAACGCTCCAACTCCCC
5342	Table 3A	Hs.171262	AI628893	4665693	ty95h02.x1 cDNA, 3' end /clone=IMAGE:2286867 /clone_end=3'	-1	TTCCCAAGTTGCCACAGACCGTTTATA TGAAGAAATGCTAAAGAAGTCCC
5343	Table 3A	NA	AI628930	4665730	ty40d03.x1 NCI_CGAP_Ut2 cDNA clone IMAGE:2281541 3' similar to SWATP6_HUMAN P00846 ATP SYNTHASE A	-1	TCTACTGACTATCCTAGAAATCGCTG TCGCCCTTAATCCAAGCCTACGTTT
5344	db mining	Hs.264154	AI630176	4681508	ad06a03.r1 cDNA /clone=ad06a03-(random)	-1	AGTTCTAAAGCCGGGAATTCTTAAGG ATATACTAAATGAGATTATGTGTGG

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5345	Table 3A	Hs.340604	AI631850	4683180	wa36h07.x1 cDNA, 3' end /clone=IMAGE:2300221 /clone_end=3'	-1	GCCTGGGGAGGAGAAAGTCCCTTCC CATTCCAGCTCGATCAATCTTGCTG
5346	Table 3A	Hs.256729	AI634652	4685982	wx27c05.x1 cDNA, 3' end /clone=IMAGE:2544872 /clone_end=3'	-1	GGAGTAGAGAGAGTCTTGCTACATGC GGGAAGTAACTTACATCATCTGCG
5347	Table 3A	Hs.319825	AI634972	4686302	602021477F1 cDNA, 5' end /clone=IMAGE:4156915 /clone_end=5'	-1	AAGAACGTTTATTGATATCCACTGGT CACATCATACCTGTCTATAAGGGCA
5348	Table 3A	Hs.176920	AI638800	4691034	tt32e01.x1 cDNA, 3' end /clone=IMAGE:2242488 /clone_end=3'	-1	TGCTTCAGCACAGGATTATGGAAT AGTTGGCAAATTAAACAAACATGCT
5349	Table 3A	Hs.197028	AI650871	4734850	602643870F1 cDNA, 5' end /clone=IMAGE:4774817 /clone_end=5'	-1	CGGCAGCCTTATGGAATGAGTTCTT GTCTGAATGTTGCCAAAGCT
5350	Table 3A	Hs.4283	AI651212	4735191	602621616F1 cDNA, 5' end /clone=IMAGE:4755315 /clone_end=5'	-1	ACAGTTACTTGGAGCTGCTAGACTG GTTCCTGTGTTGGTAATTGCCT
5351	db mining	Hs.203064	AI651922	4735901	hy16b12.x1 cDNA, 3' end /clone=IMAGE:3197471 /clone_end=3'	-1	TGTGAAGAACCTTACCAATTAAACC CTGGGTGGATAAAATAAAAATGGG
5352	Table 3A	Hs.195378	AI653766	4737745	ty01b06.x1 cDNA, 3' end /clone=IMAGE:2277779 /clone_end=3'	-1	CCCAAAATTGTTAAAGTCCGACTT CCAAAAGGGGCCAATAAAAAGGG
5353	db mining	Hs.111941	AI660405	4763975	qd92a04.x1 cDNA, 3' end /clone=IMAGE:1736910 /clone_end=3'	-1	CACCGCCTCTGCCCTCCGCCCTTCCA CTGGAGAGCCCGAGGTCAAAGGTC
5354	Table 3A	Hs.200442	AI669591	4834365	tw34b09.x1 cDNA, 3' end /clone=IMAGE:2261561 /clone_end=3'	-1	CCCTCACCTAGCAGTACTACCAAT AATGCTATCATGGTCCCAGGGAT
5355	Table 3A	Hs.101150	AI672433	4852164	Homo sapiens, clone IMAGE:4054156, mRNA, partial cds /cds=(0,526)	-1	TCTCCTTCCCCATTGGGCCGCTTA TCAATTGCCTGTTTGTGTTTGT
5356	Table 3A	Hs.341178	AI678004	4888186	xa30a04.x1 cDNA, 3' end /clone=IMAGE:2568270 /clone_end=3'	-1	TTTTTATCTTCTGGTGGGGGTG GTGGTGGTGAAGAGGACCTAAAAA
5357	Table 3A	Hs.324507	AI678099	4888281	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(182,2056)	-1	CGCCAGAGGTCAAGAACATGTCATT TGAATTGGATCGTTACAATGAGC
5358	Table 3A	Hs.178784	AI681868	4892050	602587746F1 cDNA, 5' end /clone=IMAGE:4716442 /clone_end=5'	-1	GCAGGCACTGACATTTGAGCAAAG ACGGTATGTTATGAGATAAAATAC
5359	Table 3A	Hs.90744	AI684022	4895316	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA /cds=(0,1268)	-1	TTCTGACACGATTACACAACGAGGCT TTAATGCCATTGGTAGGTGAGC
5360	db mining	Hs.328323	AI684369	4895663	tc96e09.x1 cDNA, 3' end /clone=IMAGE:2074024 /clone_end=3'	-1	TTTAAAGGGAGGGCCGGGGTT GGTCCCCGGTCCAAAGGTAAGGTT
5361	Table 3A	Hs.58774	AI684437	4895731	Homo sapiens, Similar to zinc finger protein 175, clone MGC:12651 IMAGE:4301632, mRNA, complete cds /cds=(367,522)	-1	GAGTGAGAAGAGGCTTTAAAGGACCA TGTAAAGAGGCTTTAAACACTTT
5362	db mining	Hs.182817	AI684847	4896141	602290551F1 cDNA, 5' end /clone=IMAGE:4385293 /clone_end=5'	-1	GGGTTGGATAAACTGCTTAGATGTT TGCCTACTGTCCAGTGAAATTAC
5363	Table 3A	NA	AI688560	4899854	wd39f08.x1-Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2330535 3', mRNA sequence	-1	ACTGAAAAGTTGAAAGACTTTGCAG TGAACATTATATAACTCCCCGCT
5364	Table 3A	Hs.201789	AI693179	4970519	MR1-CI0181-061100-001-a01 cDNA	-1	ATTCA TAGGTAGTGCCTCAGAGAGT ACAAGCTCTGACTCATGGCAGT
5365	literature	Hs.202407	AI697497	4985397	we14b06.x1 cDNA, 3' end /clone=IMAGE:2341043 /clone_end=3'	-1	ACATGTTACCTGGAGTAGCTGTGCA ACAGATTAATATGGAATGCTACTA
5366	Table 3A	Hs.177708	AI697756	4985656	602369210F1 cDNA, 5' end /clone=IMAGE:4477370 /clone_end=5'	-1	TGGTTCCTGTGCTCACCATAGGGCTG GTGTACATTGGGCCATTATAAAC
5367	Table 3A	Hs.206654	AI700738	4998638	EST366531 cDNA	-1	ACAGATCCCTATTGCCAGACACATCA TTCTCTCCATCCAGAAAGCAAACA
5368	Table 3A	Hs.80887	AI701165	4989065	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA /cds=(297,1835)	-1	TCTGGAAAGACATTTAAGCTGCT GACTTCACCTGCAAATCTAACAG
5369	Table 3A	Hs.102793	AI707589	4997365	RST17769 cDNA	-1	AGTCACGATAAAACCTGGTCACCTGAA AATTGAAATTGAGCCACTTCCTG
5370	Table 3A	Hs.309433	AI707809	4997585	as28g09.x1 cDNA, 3' end /clone=IMAGE:2318560 /clone_end=3'	-1	AAACTGGCGGCCAACAAAACAGTG GGTAAATGGTCCCTGGGTGACAT
5371	Table 3A	Hs.107369	AI707896	4997672	as34a10.x1 cDNA, 3' end /clone=IMAGE:2319066 /clone_end=3'	-1	AGTGTTCCTCCACATCTAAAGAAAG CCCATTGAAACTGGTACTGCA
5372	Table 3A	Hs.176430	AI708327	4998103	at04c02.x1 cDNA, 3' end /clone=IMAGE:2354114 /clone_end=3'	-1	CCCAAGGTGGCCCTCTCCATCAGAT GTTATTGCTTCCCCATTATTA

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5373	Table 3A	Hs.300710	AI709236	4999012	RC0-MT0059-200600-021-g05 cDNA	-1	AAGATGCCAAAGCGTTAACCGGGTGA AACAGGGGTGGAGAGAGAAAGAA
5374	Table 3A	Hs.297184	AI720536	5037792	601502712F1 cDNA, 5' end /clone=IMAGE:3904539 /clone_end=5'	-1	GTCATACACCTATCCCCCATTTCCT CCTATCCCTCAACCCGGACATCAT
5375	Table 3A	Hs.313929	AI733018	5054131	oh50h01.x5 cDNA, 3' end /clone=IMAGE:1471441 /clone_end=3'	-1	GCAGGTGGCAGAATGGGGTGCATGA AGGTTCTGAAAATTAAACACTGCTT
5376	Table 3A	Hs.310333	AI735206	5056730	at07f03.x1 cDNA, 3' end /clone=IMAGE:2354429 /clone_end=3'	-1	ACAGAGAGGCAGCATTGTTTCCAG TTAAAATTGACCTCACTGTGATT
5377	Table 3A	Hs.277201	AI740667	5108955	wg07b07.x1 cDNA, 3' end /clone=IMAGE:2364373 /clone_end=3'	-1	CCCCCTTTGTTGTGGTTTATATTGG AACCCCTTTCTTGGAACTA
5378	Table 3A	Hs.204656	AI741246	5109534	wg26g09.x1 cDNA, 3' end /clone=IMAGE:2366272 /clone_end=3'	-1	CTGACCCCTTCCTCACCCCTGCCAAC AGTGGTGGCATATATCACAAATGG
5379	Table 3A	Hs.299883	AI742850	5111138	hypothetical protein FLJ23399 (FLJ23399), mRNA /cds=(282, 1769)	-1	TGTTTACCTCACTGTTGGACATACAT TCCAAGCTTTCAACTCTAGGAG
5380	Table 3A	Hs.6187	AI745230	5113518	wg10e05.x1 cDNA, 3' end /clone=IMAGE:2364704 /clone_end=3'	-1	CAGAACATGCCAAAGAAGCTATAT CTTGTGCTGGAAATGTAAAGCA
5381	Table 3A	Hs.293842	AI748827	5127091	601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5'	-1	CAAACACCGGCAGTTGAAAGGAAAA GGACGGGAATGTGATGGAAAAGAG
5382	Table 3A	NA	AI749435	5127699	at24b04.x1 Barstead aorta HPLRB6 cDNA clone IMAGE:2356015 3' similar to gb:X55715 40S RIBOSOMAL PRO	-1	CCCCCTCCCTGCCCGGTGAGCTTT GGGGAACCCAAAATTAGATTTTGC
5383	Table 3A	Hs.204929	AI749444	5127708	at24c03.x1 cDNA, 3' end /clone=IMAGE:2356036 /clone_end=3'	-1	CCCAAATCCAAGGCCAACATGCTGTTG TAAACAAGGGTAAAGGGCCTAA
5384	Table 3A	Hs.205071	AI760018	5175685	wh83b02.x1 cDNA, 3' end /clone=IMAGE:2387307 /clone_end=3'	-1	ACTCCACCAAGACTGTGAACCTCCACC GGGGTAGGAAGCATATTACTCA
5385	Table 3A	Hs.160951	AI760020	5175687	wh83b05.x1 cDNA, 3' end /clone=IMAGE:2387313 /clone_end=3'	-1	GAGAACTCGTTCAAGGAACACTCGATG TTTCCGGGGACCAAGCCCAGCCAG
5386	Table 3A	Hs.340921	AI760026	5175693	wh83c05.x1 cDNA, 3' end /clone=IMAGE:2387336 /clone_end=3'	-1	CCAGCGAATTCCAGCTTTGAACT CAGATTCCCTTTGCGACCCAGGT
5387	Table 3A	Hs.26873	AI760224	5175891	wh82g06.x1 cDNA, 3' end /clone=IMAGE:2385370 /clone_end=3'	-1	GATGCGCGGCAAGAATGTACCTGTA GATGTGTACATACCACAGTGCTGTA
5388	Table 3A	Hs.14373	AI760353	5176020	yx26h11.r1 cDNA, 5' end /clone=IMAGE:262917 /clone_end=5'	-1	TTTATCTCAGAATCTTGATGAACCTG AAATGACCCCTGATGGGGCATG
5389	db mining	Hs.204598	AI760374	5176041	wh87d12.x1 cDNA, 3' end /clone=IMAGE:2387735 /clone_end=3'	-1	GGCCCCCTGTCCTTACCTGTTTCGG CCCCCTTAATTTTAACCCCCGGG
5390	db mining	Hs.283496	AI760389	5176056	wh87f08.x1 cDNA, 3' end /clone=IMAGE:2387751 /clone_end=3'	-1	GTCACAGTGTAGACACATGGTCTTC CATAGTGAGTAGAATATCCATTGT
5391	db mining	Hs.340927	AI760556	5176223	wi10d09.x1 cDNA, 3' end /clone=IMAGE:2389841 /clone_end=3'	-1	GTGGCCTGGCCTGGCTCTCACAGAC CCAAGGCTTCCGTAGAATATGTC
5392	db mining	Hs.205803	AI760674	5176341	wh96b04.x1 cDNA, 3' end /clone=IMAGE:2388559 /clone_end=3'	-1	GGATTGTGGCAGGAACCTGTTCCCT CCCAGCCTTAAATTCTGTGTT
5393	db mining	Hs.283497	AI760698	5176366	7f34c12.x1 cDNA, 3' end /clone=IMAGE:3296566 /clone_end=3'	-1	AAACCCACACCTCAGTGAATTAAAA GAGTAGATGTTAAAAGACCGGA
5394	db mining	Hs.264654	AI760835	5176502	wh96f11.x1 cDNA, 3' end /clone=IMAGE:2388621 /clone_end=3'	-1	TGCCATTGGTATTTTCTGAAACA TTACATAATAAGAATGCAGCATGC
5395	Table 3A	NA	AI760901	5176568	wi09h06.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2389787 3', mRNA sequence	-1	GCCTGAAACCATCCTGCCCTTAGGA AGACAGCAATTCTGGAGAGCAAG
5396	db mining	Hs.230931	AI760991	5176658	wh97b11.x1 cDNA, 3' end /clone=IMAGE:2388669 /clone_end=3'	-1	GGTGGTCCCCAGCCCTTCCCTGG CCCTGGGTGGAAAATTGTTTC
5397	db mining	Hs.328494	AI761029	5176696	wi10d06.x1 cDNA, 3' end /clone=IMAGE:2389835 /clone_end=3'	-1	AAAACCTTCGCCCCGGCTAAATT ACCGGGGTTGGTTTATTGGTTT
5398	Table 3A	Hs.98531	AI761058	5176725	wi69b03.x1 cDNA, 3' end /clone=IMAGE:2398541 /clone_end=3'	-1	CTCCTGGGTGTCATGCAACTGAGGAA CCTAATTGGCTGGGTGGGTTGTT
5399	Table 3A	Hs.205452	AI761141	5176808	wh97g08.x1 cDNA, 3' end /clone=IMAGE:2388734 /clone_end=3'	-1	TTTGTAAAAGAACCTGCCACATTG TTGAAAAGTTAGGCCATCACAGC

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5400	Table 3A	NA	AI761144	5176811	wh97h01.x1 NCI_CGAP CLL1 cDNA clone IMAGE:2388721 3', mRNA sequence	-1	CTCTTGGCTGCTGGCCTTTGTTCTT GTCATGGCTCATTAGCTCCCTAAA
5401	db mining	Hs.328495	AI761468	5177135	wh98e07.x1 cDNA, 3' end /clone=IMAGE:2388804 /clone_end=3'	-1	CCAGGGGTTTTAAATTTCTGAAGTT TTTGGGCCATTGGTTGTGG
5402	Table 3A	Hs.80887	AI761622	5177289	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA /cds=(297,1835)	-1	CCCCGCTTGCTTTATTCAGAACCC CCAAGTATTACCCAATATGTTACA
5403	Table 3A	Hs.289834	AI761924	5177591	wg58h03.x1 cDNA, 3' end /clone=IMAGE:2370293 /clone_end=3'	-1	GCCGAAGCTCACAGAGGCTAAGTTA CACGCTTAGGTGTTATTCTAC
5404	Table 3A	Hs.204610	AI762023	5177690	wh89f04.x1 cDNA, 3' end /clone=IMAGE:2387935 /clone_end=3'	-1	AACCAGGTTATGATGCTGTAATAAA CCATGGCATTAAAGAGGGCAAGAG
5405	db mining	NA	AI762158	5177823	wh90e05.x1 NCI_CGAP CLL1 cDNA clone IMAGE:2388032 3' similar to gb:X64707 BREAST BASIC CONSERVED PR	-1	GGGTTAAGGAGGGCCGCTCCAAAT TTTCCCTTTCCAGGAAGCCCTTG
5406	db mining	Hs.204771	AI762177	5177844	wh90g09.x1 cDNA, 3' end /clone=IMAGE:2388064 /clone_end=3'	-1	ATGCTGTGAGTGTTACACATGGCTGA GGTTATGATCTGTTAAATATGTA
5407	Table 3A	Hs.205327	AI762557	5178224	wh92f07.x1 cDNA, 3' end /clone=IMAGE:2388229 /clone_end=3'	-1	TTCATTAATTCTCAACCCAATACTGT CTGGCTTCCACCAACAGGAGCGGG
5408	db mining	Hs.328503	AI762707	5178374	wh93d06.x1 cDNA, 3' end /clone=IMAGE:2388299 /clone_end=3'	-1	TGGTTTCTATTTAAAAACCTGGGTTA GCCAAGGTTGGGTTGCCCT
5409	db mining	Hs.204477	AI762719	5178386	wh93e10.x1 cDNA, 3' end /clone=IMAGE:2388330 /clone_end=3'	-1	CAACATTGCCCTACCAAGTTGCAGTTCA TTAGCCCCGTCCGCCCCAGCATTG
5410	db mining	Hs.205815	AI762739	5178406	wh93g11.x1 cDNA, 3' end /clone=IMAGE:2388356 /clone_end=3'	-1	CCTTGGGGTGGGGCTTTCCCTTT TTGGCCGGTCAATTAGGTTTT
5411	Table 3A	NA	AI762741	5178408	wh93h02.x1 NCI_CGAP CLL1 cDNA clone IMAGE:2388339 3', mRNA sequence	-1	CCCACTCCGGCTTTAGAAGTTT CCCGAATCCGTATCCCTTACAA
5412	db mining	NA	AI762797	5178464	wi04c12.x1 NCI_CGAP CLL1 cDNA clone IMAGE:2389270 3' similar to TR:Q61655 Q61655 EUKARYOTIC TRANSLA	-1	AATGGGCAAATTACCCAAACCTTA AGCTTGCCTATTCCGTTGAGGCA
5413	Table 3A	Hs.333513	AI762870	5178537	wi63c07.x1 cDNA, 3' end /clone=IMAGE:2397996 /	-1	GAAGGAGAGGCACACACAAATACAC ACACACACAAACTCAACACCA
5414	db mining	Hs.204480	AI762931	5178598	wh94e08.x1 cDNA, 3' end /clone=IMAGE:2388422 /clone_end=3'	-1	GGATACCCCTTTATCCCGAGGGAAT TTTACCCCTTGATGCCCTTAA
5415	db mining	Hs.289836	AI762955	5178622	wh94g12.x1 cDNA, 3' end /clone=IMAGE:2388454 /clone_end=3'	-1	CAAATTACAAACCTAAAAATACAGAA CATCAGCGGACAAGACAGGAGAGC
5416	db mining	Hs.277238	AI763079	5178746	wh95a12.x1 cDNA, 3' end /clone=IMAGE:2388478 /clone_end=3'	-1	CTCCTCCCTGGGTGGGACCTGGGT TGGGGGTTGATAGAAAATTAAACC
5417	Table 3A	Hs.173904	AI763121	5178788	wi06d12.x1 cDNA, 3' end /clone=IMAGE:2389463 /clone_end=3'	-1	GGTTAAACTAGATCCCTGCAAGGCCA TCACCTCCATTCAAAGTTGTTACT
5418	Table 3A	Hs.190453	AI763206	5178873	wh95e09.x1 cDNA, 3' end /clone=IMAGE:2388520 /clone_end=3'	-1	AGTGGGTTATTTAGATCTTCTCTG GGGTCAGGTACATAGCTTAAC
5419	db mining	Hs.283500	AI763225	5178892	UI-H-BW1-anj-a-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082282 /clone_end=3'	-1	TGTTGGGTATATTGTTGGGTTTG GCCACTAGGATGGGTGACTCAGGG
5420	Table 3A	Hs.130059	AI763262	5178929	wi66c04.x1 cDNA, 3' end /clone=IMAGE:2398278 /clone_end=3'	-1	GCCAGTGAATCTAGTTGGCTATTTC TGTTTTGTCCAGTTTCCCAT
5421	db mining	Hs.328504	AI763414	5179081	wh92a11.x1 cDNA, 3' end /clone=IMAGE:2388188 /clone_end=3'	-1	AACCATTTCCCCGGGACCCGTT TGCCTGGTTCGATTTTACCC
5422	Table 3A	Hs.36137	AI765153	5231662	hepatocyte nuclear factor 3, gamma (HNF3G), mRNA /cds=(0,1043)	-1	CCGGGAAGCGGGGTACTGGCTGT TTAATCATTAAAGGTACCGTGTCCG
5423	db mining	Hs.340947	AI766625	5233134	wi0106.x1 cDNA, 3' end /clone=IMAGE:2388995 /clone_end=3'	-1	TTTTCCCCCTCCCAAATTCACTGCAT TACAGTTTGAAACAGAACGGG
5424	Table 3A	NA	AI766838	5233147	wi02a10.x1 NCI_CGAP CLL1 cDNA clone IMAGE:2389050 3', mRNA sequence	-1	TACGAGAAGTCAGGAAGTTGAAAT GGCAGTGACAGGAGACGGGGAAAG
5425	db mining	Hs.210276	AI766656	5233165	wi02d04.x1 cDNA, 3' end /clone=IMAGE:2389063 /clone_end=3'	-1	AAGGGCAGGCAAATCAATTAAATTA GCCGTAACAAACACCTCGGGGGTG
5426	Table 3A	Hs.223935	AI766706	5233215	wi02g11.x1 cDNA, 3' end /clone=IMAGE:2389124 /clone_end=3'	-1	AGTACACGGCCCTCAAAAGTTATG TGCTGAATGTAACCTACTTAGCGA

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5427	Table 3A	Hs.89104	AI766963	5233472	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	TTGTTTTAACAACTCTTCAACATTT TGTCAGGTATTCACTGTAACCA
5428	Table 3A	Hs.209511	AI768880	5235389	wh71e04.x1 cDNA, 3' end /clone=IMAGE:2386208 /clone_end=3'	-1	CTTCTCCACCTCGGCCAGGTATAGG GCCAGCTTCTCGTCTCTGGGATCCG
5429	Table 3A	Hs.203594	AI796317	5361780	uncharacterized gastric protein ZA43P mRNA, partial cds /cds=(0,134)	-1	GCCAGGTCAATTGTATAAGGGAGTAAGA TGAAGGTGAATTGCAGCTAGTTG
5430	Table 3A	Hs.230939	AI786419	5361882	wj17f02.x1 cDNA, 3' end /clone=IMAGE:2403099 /clone_end=3'	-1	TGTGTTTGTGTTCTGGTCCCAGGG CACCGTTGTTTGTGAACCTCCTC
5431	db mining	Hs.291079	AI797561	5363033	602437732F1 cDNA, 5' end /clone=IMAGE:4555638 /clone_end=5'	-1	CATGGCTCTAAATTTGGAAATTAACTT CTCTTGCCTTAAAGAGCTGCTTGT
5432	Table 3A	Hs.159577	AI797788	5363260	wh78b11.x1 cDNA, 3' end /clone=IMAGE:2386845 /clone_end=3'	-1	GCTGGTGGGAAGTTGAGCCATGTTA TCTCTAGTGAATCCTTACCTTGT
5433	db mining	Hs.207473	AI797813	5363370	wh79c04.x1 cDNA, 3' end /clone=IMAGE:2386950 /clone_end=3'	-1	CATGTTTACACAAATTCTTCAAGC CCCTTAAACATGGGGCCGGCCCC
5434	db mining	Hs.171110	AI797852	5363409	7e88g03.x1 cDNA, 3' end /clone=IMAGE:3292276 /clone_end=3'	-1	ACCTTAATAGCTAGGCTGGGTATATT TTCAAAGTGTAGCGAACCCCCACG
5435	db mining	NA	AI797901	5363296	wh78f12.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2386895 3' similar to contains Alu repetitive element; m	-1	CAGTTGGCCTCCATAACATTGGAAATT CTACCAAGCTCCAAGTGTGACCTGG
5436	db mining	Hs.226571	AI797916	5363311	DKFZp434G046_s1 cDNA, 3' end /clone=DKFZp434G046 /clone_end=3'	-1	GGATTCCCGACAAGGGCTTGATGTGT ACTTGAAGTGAGCAAAGGGTTTG
5437	db mining	Hs.223520	AI797988	5363460	wh80a02.x1 cDNA, 3' end /clone=IMAGE:2387018 /clone_end=3'	-1	GGGTGGAGACAGGCTAATCCTTTC CCCTTGTTCACGTCCTTATGAC
5438	db mining	Hs.207062	AI798027	5363499	wh80e09.x1 cDNA, 3' end /clone=IMAGE:2387080 /clone_end=3'	-1	ACAACCTCTTAATATATTAGAGACCC GCAGGAAACATTAGTGGTAAAC
5439	db mining	Hs.341012	AI798028	5363500	wh80f11.x1 cDNA, 3' end /clone=IMAGE:2387085 /clone_end=3'	-1	GTACATGTTGTGCTAAATTGCTC ATTGGCAGTGATAGATTGAAAAAC
5440	db mining	Hs.229494	AI798100	5363583	wh81d01.x1 cDNA, 3' end /clone=IMAGE:2387137 /clone_end=3'	-1	GGGGTCAAAGAGGGTACAAATGTA TGGGGTATAATGAAATGCTAACAT
5441	db mining	Hs.328535	AI798101	5363584	wh81d02.x1 cDNA, 3' end /clone=IMAGE:2387139 /clone_end=3'	-1	GGGAGCCCGTTAGAAGGAAGGGC AAAAGTAGGTTTTAACCAAACG
5442	db mining	Hs.210307	AI798114	5363576	wh81c01.x1 cDNA, 3' end /clone=IMAGE:2387136 /clone_end=3'	-1	TCCGTCCCATTCCCCCGAAAACAAG GTTTGAATTGGCCCGTAAAGGG
5443	Table 3A	Hs.209609	AI798144	5363616	wh81g12.x1 cDNA, 3' end /clone=IMAGE:2387206 /clone_end=3'	-1	ACGTCTTATAACATGCACTGTTGA TTTTAACAAACATCTGAAGGGCT
5444	Table 3A	Hs.158989	AI799909	5365381	602666595F1 cDNA, 5' end /clone=IMAGE:4806358 /clone_end=5'	-1	ACTCAATACTCGGGAAAGGCTTCACA TTCTGGGACTCAGCATTATCCAA
5445	Table 3A	Hs.135167	AI802181	5367664	AV712376 cDNA, 5' end /clone=DCAAAND12 /clone_end=5'	-1	TTGAGAGGCAACACTAAACACTAGG GCTACTGTGGCATCTATGAGACA
5446	Table 3A	Hs.195175	AI802547	5368019	mRNA for CASH alpha protein /cds=(481,1923)	-1	AGCCCTTTCTTGTGCTGTATGTTA GATGCTTCCAACTTTGTACT
5447	Table 3A	Hs.25648	AI803065	5368537	tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), mRNA /cds=(47,880)	-1	GGGTATGGTTAGTAATATCCACCA GACCTCCGATCCAGCAGTTGGT
5448	Table 3A	Hs.301209	AI804629	5370101	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (MLLT10), mRNA /cds=(183,3266) tc90g10.x1 cDNA, 3' end /clone=IMAGE:2073474 /clone_end=3'	-1	AACAAACAACAGCAAAATCCCTTAGT GCGTAACTTGAATTCCCTCGGC
5449	db mining	Hs.209261	AI805106	5391760	tc90g10.x1 cDNA, 3' end /clone=IMAGE:2073474 /clone_end=3'	-1	TTGTAAGTGGGTGCATAAGAAGATCT CTTCAATTAAATGCCCGCTGGT
5450	Table 3A	Hs.187698	AI805111	5391765	cytomegalovirus partial fusion receptor mRNA, partial cds /cds=(0,1037)	-1	ATAATTAAAGAAATCAGCCGTGTGCTT CTCACGTTGGCTCCGAGACGTG
5451	Table 3A	Hs.167208	AI805131	5391785	602727149F1 cDNA, 5' end /clone=IMAGE:4866348 /clone_end=5'	-1	GTCAGTCTCCTCACCTGCTCTGCTC CTCGCTTAGCCATTGATTGATC
5452	db mining	NA	AI805144	5391798	td11g08.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2075390 3' similar to gb:L24038_ma1 A-RAF PROTO-ONCOGENE	-1	GGGAAGAAGCCCGTCCCCCACCA ATAAAATGTTGGTTTGGCCCTGATG
5453	db mining	NA	AI805257	5391750	tc90f09.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2073449 3', mRNA sequence	-1	CAGAACTTCTGGCGAAGGCCATGTAA GAACTACTCCAAGGAGGAAGAGGC

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5454	Table 3A	NA	AI807278	5393844	wf38h03.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2357909 3', mRNA sequence	-1	CTCTACCATAAGGCACATCACAGAGAC TGCTACTGGAGTGATATTGGTT
5455	db mining	NA	AI808039	5394527	wf52h02.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2359251 3' similar to TR:Q62845 Q62845 NEURAL CELL	-1	ACTGCTACAGCTAACCATTTGTCGA AGCTAATTAAATTACCTTGGGGA
5456	Table 3A	Hs.87912	AI808931	5395497	EST379776 cDNA	-1	CAATTGTGATTTGGAAAGGTTAACGT GGTCTGCCAGATGTTACGAATA
5457	db mining	Hs.209989	AI809181	5395747	wh75d05.x1 cDNA, 3' end /clone=IMAGE:2386569 /clone_end=3'	-1	TCCAAAGCAAAAGTTATGCAATAAGAC AGAATATAAAGTCTCCGAGAGCCT
5458	db mining	Hs.230485	AI809184	5395750	wh75d08.x1 cDNA, 3' end /clone=IMAGE:2386575 /clone_end=3'	-1	GGGTGGGGTGGGGTGAGAGTGTGTG GAGTAAGGACCTTCAGAATTAAAT
5459	db mining	Hs.292761	AI809305	5395871	wh75g11.x1 cDNA, 3' end /clone=IMAGE:2386628 /clone_end=3'	-1	TGCAAGTTCTTATTCTTTGCCTGTG ATAATTGCAAATCCGTCATAGAA
5460	Table 3A	Hs.210385	AI809310	5395876	wh75h08.x1 cDNA, 3' end /clone=IMAGE:2386623 /clone_end=3'	-1	TGCAAGTTCTGAGACTGTGAAAAGT GTTTGCTCTTTGTTACCCAAT
5461	db mining	Hs.90463	AI809378	5395944	wa27e12.x1 cDNA, 3' end /clone=IMAGE:2299342 /clone_end=3'	-1	TCCCAAGCGAATGTGAATCATTAGTG TGCTACTCAAATTAGGTGTCCAC
5462	Table 3A	Hs.257466	AI809475	5396041	UI-H-B13-ald-e-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2736471 /clone_end=3'	-1	TAAGATGTAGGGGCCACCGGGCAGC AGTACCCAGCAATGACCACTATCAG
5463	db mining	Hs.208153	AI809564	5396130	wh76e01.x1 cDNA, 3' end /clone=IMAGE:2386680 /clone_end=3'	-1	ATAATGAAAGCATACCAAGTGTGT CCATTCAGGTACAACATATGGAA
5464	db mining	Hs.310486	AI809746	5396312	7e96g11.x1 cDNA, 3' end /clone=IMAGE:3293060 /clone_end=3'	-1	CTGGTATTCTGAGGTCAAGATGTAGGC TGTTGCTCGCTCCGGCTGGGTCTC
5465	Table 3A	Hs.277293	AI811065	5397631	tr03f05.x1 cDNA, 3' end /clone=IMAGE:2217249 /clone_end=3'	-1	CCATCGGGGGTATTGGGGTTTGGG CTGAATTACTGATTATGGAAAA
5466	Table 3A	Hs.86693	AI81153	5436320	EST380760 cDNA	-1	GCCAGATTGTGGCAGGTAAAGAGAC AATGTAATTGCACTCCCTATGATA
5467	Table 3A	Hs.230492	AI818596	5437675	wk74d04.x1 cDNA, 3' end /clone=IMAGE:2421127 /clone_end=3'	-1	TTTAAAAGGAGGGAGGGATTCTGGG TAAACACTTTATTGGCCCCCAT
5468	Table 3A	Hs.229990	AI818777	5437856	wl11f10.x1 cDNA, 3' end /clone=IMAGE:2424619 /clone_end=3'	-1	TAAAACCCAAGACTTCAGATTAGCC GAATTGTGGTTTACAAGGCGC
5469	Table 3A	NA	AI818951	5438030	wj89e12.x1 NCI_CGAP_Lym12 cDNA clone IMAGE:2410030 3' similar to WP:C11H1.7 CE18492 ;contains Alu r	-1	CTAACATGGGAAGGGGGCAGAGT GAGGACTGTGCCATTGATTAAAGTG
5470	Table 3A	Hs.51039	AI823541	5444212	KIAA0076 gene product (KIAA0076), mRNA /cds=(86,5182)	-1	GTACAGAAAACATATTCCATGCTTGA AATAAAGGGAAGTGCTCCCTGTT
5471	Table 3A	Hs.211535	AI823649	5444320	wi85g03.x1 cDNA, 3' end /clone=IMAGE:2400148 /clone_end=3'	-1	GAAGCCTTTCTTTCTGTTACCCCTC ACCAAGAGCACAACTTAAATAGG
5472	Table 3A	Hs.304477	AI824522	5445183	bx71d03.x1 cDNA, 3' end /clone=IMAGE:2275013 /clone_end=3'	-1	ACCGATCGTTTTAGGATAATGCA TGTTCAAGTGGTATTGAAACCCCC
5473	db mining	Hs.270624	AI825096	5445859	7b65e05.x1 cDNA, 3' end /clone=IMAGE:3233120 /clone_end=3'	-1	TGAGGGACAGGCTGCCTAAAGCTAA TTGGAGAGTAACTTAATGTCGT
5474	Table 3A	Hs.117906	AI825645	5446316	wb75b09.x1 cDNA, 3' end /clone=IMAGE:2311481 /clone_end=3'	-1	CACCATCGTGGCTCTGAGAACCTGAC GCCGTGAATGTTGACCTGAGTGCCG
5475	Table 3A	Hs.229993	AI827451	5448122	wl17d11.x1 cDNA, 3' end /clone=IMAGE:2425173 /clone_end=3'	-1	GGGGAGAGACCACCCTAGACATTG CATTTTGTAAAGTTAGCCAGCCAAT
5476	Table 3A	Hs.181400	AI827911	5448669	602650370T1 cDNA, 3' end /clone=IMAGE:4781353 /clone_end=3'	-1	TGGATAAACTGAGCAACTTCTCTT TGTGCTCAGGAACCTACGCACT
5477	Table 3A	Hs.342617	AI827950	5448708	ha15h10.x1 cDNA, 3' end /clone=IMAGE:2873827 /clone_end=3'	-1	TGTGGGTTTGTATTGACATACTGTT TTCATGCTGAAGTTGAGTGTCTG
5478	Table 3A	Hs.132238	AI829569	5450240	wf28e02.x1 cDNA, 3' end /clone=IMAGE:2358922 /clone_end=3'	-1	GGTGTGCAGTCGCCCTGAAAGCCTT CCCCTTAGCTATTAGGAATTGAGTC
5479	db mining	Hs.289878	AI831819	5452490	wh84f12.x1 cDNA, 3' end /clone=IMAGE:2387471 /clone_end=3'	-1	ACATTGGAAAGAAACCCCTACAACGT AATGAATATGAAAAGAATTGCTAAAA
5480	Table 3A	Hs.341177	AI832038	5452709	wj99e02.x1 cDNA, 3' end /clone=IMAGE:2410970 /clone_end=3'	-1	AAAACCGTTTCCCCATACATAAAGA ACAGGGGACTCCCGCCCTGATGG

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5481	Table 3A	Hs.210995	AI832182	5452853	td13h11.x1 cDNA, 3' end /clone=IMAGE:2075589 /clone_end=3'	-1	TTTGGTGAAGTGAAGAGAGAAAGTTG CTCTAAAAGGTGGAAACCAGCCC
5482	Table 3A	Hs.249031	AI832183	5452854	wh80g09.x1 cDNA, 3' end /clone=IMAGE:2387104 /clone_end=3'	-1	TGGACTGTTGTAATGTTTGCGTTAT CAAAATGAAAATGCCAAATGAGA
5483	Table 3A	Hs.63908	AI858771	5512387	hypothetical protein MGC14726 (MGC14726), mRNA /cds=(21,653)	-1	GCTTGAGTTTGGGATGGTCACATG ACACAATCCAGCACTTGAAACCTGA
5484	Table 3A	Hs.252259	AI859076	5512692	ribosomal protein S3 (RPS3), mRNA /cds=(22,753)	-1	AGAGCCATTCCACAAAGTAAATGTG CAGTCCCCATGTTCTTGTGTTA
5485	Table 3A	NA	AI860120	5513736	wh39e01.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2383128 3', mRNA sequence	-1	GACTCTGAGAGAGAGCAGCGCAT CATAGAACAGCGAAGGCAGTCGATC
5486	db mining	Hs.156811	AI862332	5526439	hz33g10.x1 cDNA, 3' end /clone=IMAGE:3209826 /clone_end=3'	-1	ATCGATGAGAAGAGTCTGCAAACAC TTTCATCCTCAGGACGTGCTGTCCT
5487	db mining	Hs.304508	AI862585	5526702	wh99g01.x1 cDNA, 3' end /clone=IMAGE:2388912 /clone_end=3'	-1	ATATATTAACACACAGGTATTAGAGA CATGAATTGCACCCAACACAAGCT
5488	Table 3A	NA	AI862623	5526730	wh99h10.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2388931 3', mRNA sequence	-1	ATTCATTGGGTCTTCCTTCTCCG CCCCTTCCATTGGCACCTC
5489	Table 3A	Hs.181426	AI865427	5529523	EST367815 cDNA	-1	TCACTTTGTGGAATCTGGTGTTC ACTATAGGTTAAGAGTGGCATT
5490	Table 3A	Hs.341208	AI865603	5529710	wk47g03.x1 cDNA, 3' end /clone=IMAGE:2418580 /clone_end=3'	-1	TGTGTTGGGGGTGCTTTGAGGTT GGAGGAAAGTAGAGACAGCGAAC
5491	Table 3A	Hs.9788	AI866194	5530301	hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5 (MGC10924), mRNA /cds=(104,769)	-1	TGTGTTTTGCCAAGTGGTAATTCA TCTGGTTTGCTATGTTAAACT
5492	Table 3A	Hs.224760	AI874107	5548156	wm49b01.x1 cDNA, 3' end /clone=IMAGE:2439241 /clone_end=3'	-1	CTTGGGGACCTAAACCCCAGGTGG TCTCTGGTGTAAATAATGCTGGAA
5493	Table 3A	NA	AI880542	5554591	at80h05.x1 Barstead colon HPLRB7 cDNA clone IMAGE:2378361 3' similar to SW:ATP6_HUMAN P00846 ATP SY	-1	AAATCGCGGTGCCCTAAATCCAAGCC TAGGTTTACACTTTAGTAAGC
5494	Table 3A	Hs.220850	AI880607	5554658	ym91d11.r1 cDNA, 5' end /clone=IMAGE:166293 /clone_end=5'	-1	TGGGGCACTTTGAAAACCTCACAGGC CCACCTGCTGCTTGCTGAATAAAA
5495	Table 3A	Hs.89414	AI884548	5589712	chemokine (C-X-C motif), receptor 4 (fusin) (CXCR4), mRNA /cds=(88,1146)	-1	GACATTCATCTGTTCCACTGAGTCT GAGTCCTCAAGTTTCACTCCAGC
5496	Table 3A	Hs.23096	AI884671	5589835	602254146F1 cDNA, 5' end /clone=IMAGE:4346626 /clone_end=5'	-1	TGGCAGGGATAAATAGAGGCATTGTT TTTCTACTTGATATCATTTGGC
5497	db mining	Hs.34650	AI885574	5590738	602286784T1 cDNA, 3' end /clone=IMAGE:4375724 /clone_end=3'	-1	TGGCTCTCCTCTTGTAATATACAGG GTGAACACTTTACTGATAACACACA
5498	Table 3A	Hs.121572	AI886313	5591477	EST387650 cDNA	-1	CCAGTGTCCATGGGTGCTAGGC TGAATTATTGTAAATTGTGCTTAGG
5499	Table 3A	Hs.213385	AI912585	5632440	we11d07.x1 cDNA, 3' end /clone=IMAGE:2340781 /clone_end=3'	-1	ACCGTCTTGTGATCCCTGGAAAC CCTTAATTCAATAGTCCCTGACTGA
5500	Table 3A	Hs.228486	AI917348	5637203	ts83d10.x1 cDNA, 3' end /clone=IMAGE:2237875 /clone_end=3'	-1	AGCCCTGGGTAGCCAAGTGGATTTCC CATTCCCAAAGTTAGTAAACCTTT
5501	Table 3A	Hs.179391	AI917642	5637497	wi52d11.x1 cDNA, 3' end /clone=IMAGE:2393877 /clone_end=3'	-1	GCAGGAAAGATGGGGTGGTGGACTG TTTTGCCACTTTTGTTTGAA
5502	Table 3A	Hs.337286	AI922889	5658853	wn84g11.x1 cDNA, 3' end /clone=IMAGE:2450276 /clone_end=3'	-1	CCCCCTGAAACTGGCATTTGTAAT GTGGTTGACTTTTGATGTT
5503	Table 3A	Hs.212553	AI922921	5658885	wn81c05.x1 cDNA, 3' end /clone=IMAGE:2452232 /clone_end=3'	-1	ACCTGGGAAATCCCTAAGGGCAAAG CAAGGTAACAGGGACTTCAGTTT
5504	Table 3A	Hs.58643	AI926251	5662139	602438603F1 cDNA, 5' end /clone=IMAGE:4564968 /clone_end=5'	-1	GCCTCAGTACAAAGGGGCTTGGGA AGTGTGTTGGCTGAATAAAGGAA
5505	Table 3A	Hs.40328	AI927454	5663418	nab63b04.x1 cDNA, 3' end /clone=IMAGE:3272383 /clone_end=3'	-1	ACCCATGCCAATGAAGAACGTGTTA AAGATGAGGAGGAGAGATGTACCA
5506	db mining	Hs.154366	AI934956	5673826	ng40b06.s1 cDNA, 3' end /clone=IMAGE:937235 /clone_end=3'	-1	GCACATTCCCTCCCTATATCCTGGAA GCACCCAGATATTCTTCATGTCCTC
5507	Table 3A	Hs.101370	AI936516	5675386	AL583391 cDNA /clone=CS0DL012YA12-(3-prime)	-1	TTAACGTCATCTGCTGAGCACTGTC GTGTCACCTCCCTAGGTAACC
5508	Table 3A	Hs.180446	AI948513	5740823	importin beta subunit mRNA, complete cds /cds=(337,2967)	-1	CAGGGTATCAGATATTGTGCTTGTG CTCAGGTTCAAAGTCAGTGCC
5509	Table 3A	Hs.71245	AI954499	5746809	zl1711.1 cDNA, 5' end /clone=IMAGE:502221 /clone_end=5'	-1	TGTTAATAGTGTGACTCCAGGGAA GAACAGATGGGTGCCAGAGTGAAA

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5510	Table 3A	Hs.118820	AI955314	5747624	Homo sapiens, clone IMAGE:3357862, mRNA, partial cds /cds=(0,325)	-1	TCAAGTATACCATTTAAATATTCAT CAGGCAGAGCCCTGACCAGGAAA
5511	db mining	NA	AI961962	5754664	wt40g09.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2509984 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION	-1	CTTTCCGGTGGCCCGAGGATGCTTG GGAAGGAACCGCTCCCTTC
5512	Table 3A	Hs.341528	AI962127	5754840	wx77f07.x1 cDNA, 3' end /clone=IMAGE:2549701 /clone_end=3'	-1	TCCCCAACCCCTTAAAGGTTTTA AATTGTTCAAATCTGGCAAGTT
5513	Table 3A	Hs.37121	AI968387	5765205	phospholipase C, beta 3 (phosphatidylinositol-specific) (PLCB3), mRNA /cds=(0,3704)	-1	GACTCGGAGAGGCCAGGAGGAAACA CGCAGCTCTGAACGGCTGAGCGAG
5514	db mining	Hs.13034	AI969716	5766534	hv63f09.x1 cDNA, 3' end /clone=IMAGE:3178121 /clone_end=3'	-1	CTGTTGTGAATCATTGTGCTTTTC AACTGTCTTCAGAGGAAAGGTA
5515	Table 3A	Hs.193247	AI978581	5803611	hypothetical protein DKFZp434A171 (DKFZp434A171), mRNA /cds=(113,2584)	-1	AAGAAGCAACCCACAGCTAATTTAGA ACATGCACTCTGACAGAAAAGACA
5516	Table 3A	Hs.153	AI984074	5811293	ribosomal protein L7 (RPL7), mRNA /cds=(10,576)	-1	GCTTTGAGGACCTTCTGGAGGAAA GAAAAAGCCTGTTTGGGAGTCT
5517	Table 3A	Hs.7557	AL042081	5421426	FK506-binding protein 5 (FKBP5), mRNA /cds=(153,1526)	-1	AGGCTGCATATGGATTGCCAACGTCAG CATATGAGGAATTAAAGACATTGT
5518	Table 3A	Hs.133262	AL044498	5432716	DKFZp434l082 cDNA, 3' end /clone=DKFZp434l082 /clone_end=3'	-1	AAGACTAGAGCTACACTAGGGCACTA TCTTATTACACGACAGCACAAACAT
5519	Table 3A	Hs.39911	AL138429	6855110	mRNA for FLJ00089 protein, partial cds /cds=(62,1111)	-1	TTAAGAACCCCAAAGATTAAAGAAA CAATGTTAAGGGCTTTGTGAGGA
5520	Table 3A	Hs.89986	AL515381	12778874	cDNA /clone=CL0BB017ZH08-(3-prime)	-1	CGGAAGTCGAAATCAAATCTATGCTT TTAATTGAAACCGTGCCTGAAACG
5521	Table 3A	Hs.9096	AL520535	12784028	hypothetical protein FLJ20473 (FLJ20473), mRNA /cds=(57,1472)	-1	TCTTCACCAGGTTCAAGCTCCGTGGG CCACACTGCTGCTGTGCCAACAG
5522	Table 3A	Hs.13144	AL521097	12784590	HPSC160 protein (HSPC160), mRNA /cds=(53,514)	-1	GATAACACTGTCAGGCCAGGTCCAG GCCCTAGGTTCTTACTCTAGCTAC
5523	Table 3A	Hs.118142	AL522477	12785970	AL522477 cDNA /clone=CS0DB008YK14-(3-prime)	-1	TGGAATTACTAAATTGTGAAATTAAAC GTAACCGAAGCAACAAACGGCAA
5524	Table 3A	Hs.295112	AL528020	12791513	KIAA0618 gene product (KIAA0618), mRNA /cds=(1041,4040)	-1	GCGGGAGGCTGGGACTTTCCATTAC AAATAGAGACTTCATTCTGTTGAG
5525	Table 3A	Hs.26670	AL540260	12870241	AL540260 cDNA /clone=CS0DF032YF03-(3-prime)	-1	ACTCAGGTGGTCTGGTGTAGTGT GCTGGAGAAGAGAATTACTGGT
5526	Table 3A	Hs.285013	AL543900	12876379	putative HLA class II associated protein I (PHAP1), mRNA /cds=(148,897)	-1	CAGGTGCTTCGTGTCCTCTCTG GTTGTCTTAAAGTGACGTGTAAT
5527	Table 3A	Hs.183232	AL561892	12909772	hypothetical protein FLJ22638 (FLJ22638), mRNA /cds=(12,476)	-1	AAACACAGCCCCCCCCATTTCAGACC GCCTTCTGAGGAGAAAATGACAG
5528	Table 3A	Hs.21812	AL562895	12911771	AL562895 cDNA /clone=CS0DC021YO20-(3-prime)	-1	GCTAACTGGATAAAAGTTGTGAGAC ATTCTGAGTGACGATATTGACC
5529	Table 3A	Hs.21812	AL562895	12911771	AL562895 cDNA /clone=CS0DC021YO20-(3-prime)	-1	GCTAACTGGATAAAAGTTGTGAGAC ATTCTGAGTGACGATATTGACC
5530	Table 3A	Hs.181165	AL565736	12917408	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(53,1441)	-1	AGCTGGCTTCACTGCTCAGGTGATTA TCCTGAACCACCAAGGCCAAATAAG
5531	Table 3A	Hs.77393	AL567986	12921892	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPS), mRNA /cds=(114,1373)	-1	AGTCAGGACTGTCTAGGTCAAGGAA GCCAAGATGTCTGAAGAGAGGAA
5532	Table 3A	Hs.13256	AL570416	12926702	AL570416 cDNA /clone=CS0DI020YK05-(3-prime)	-1	ATTCACCACTGAAATGGTACCTGAGGA ATGAAATGGTATTGTTCTGT
5533	Table 3A	Hs.180546	AL571386	12928831	AL571386 cDNA /clone=CS0DI009YL09-(3-prime)	-1	AGTGGAGAGGCCCTGTTAGTTACTT TTGATATTGAGTGATGCTGAGGT
5534	Table 3A	Hs.21732	AL573787	12933363	AL573787 cDNA /clone=CS0DI055YM17-(3-prime)	-1	GCATCTTATTTAAAAAGGGAGTGGGG AGCAAAATGAAAAATTAAATGTGGGG
5535	Table 3A	Hs.23294	AL574514	12934790	hypothetical protein FLJ14393 (FLJ14393), mRNA /cds=(60,1454)	-1	TCACCAGGAAAACATGCTGTGAATT GTGCAAGTAAAAGGTGGTAATGACT
5536	Table 3A	Hs.181392	AL575666	12937052	major histocompatibility complex, class I, E (HLA-E), mRNA /cds=(7,1083)	-1	CCTTTCTCCTCCATGACCCCTTAACA GCATGCTTCATTCCCCTCAC
5537	Table 3A	Hs.85258	AL575755	12937231	CD8 antigen, alpha polypeptide (p32) (CD8A), mRNA /cds=(65,772)	-1	CTGAGAGCCCAAACGTGTCCTCCAAA CATGCACTTCCCTGCTTAAGGTAT
5538	Table 3A	Hs.169810	AL576149	12938006	mRNA for transmembrane glycoprotein (CD44 gene) /cds=(178,2406)	-1	TGAGTGAACAAAGCTGTGAAACATTG TGCGTTATGCAACTTCCCTGCC
5539	Table 3A	Hs.174905	AL577970	12941605	mRNA for KIAA0033 gene, partial cds /cds=(0,1008)	-1	CAAGAAGACAAGCATCTGTTGCG GAGGCAAGCAGGCTAACCTAGGAGTT
5540	Table 3A	Hs.5057	AL578975	12943566	AL578975 cDNA /clone=CS0DK012YN01-(3-prime)	-1	TTGGCCCACTGTGATTGATTGCTTA TCTTTGGTACTTTACTTGAATGG
5541	Table 3A	Hs.279555	AL582047	12949649	AL582047 cDNA /clone=CS0DL003YD01-(3-prime)	-1	CATCCAGCACTAATTTCATGCTTAA TGAAGAGATGCTGAGGACCTT
5542	Table 3A	Hs.198296	AL582354	12950255	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), mRNA /cds=(297,5015)	-1	AGCCTGAGGCAAATAAAATCCAGTA ATTCGAAGAATGGGTGTTGGCAA

Table 8

5543	Table 3A	Hs.101370	AL583391	12952309	AL583391 cDNA /clone=CS0DL012YA12-(3-prime)	-1	AGGACCTTGACAAGCCGTTGAGATG GAATGTAGGCCCTGATGTTATGCT
5544	Table 3A	Hs.101370	AL583391	12952309	AL583391 cDNA /clone=CS0DL012YA12-(3-prime)	-1	AGGACCTTGACAAGCCGTTGAGATG GAATGTAGGCCCTGATGTTATGCT
5545	Table 3A	Hs.7187	AU158636	11020157	mRNA for KIAA1757 protein, partial cds /cds=(347,4576)	-1	AGTGGAGTGTITACACCTTGCTGTAA CATTGAACCTTCACAAGAGATGT
5546	Table 3A	Hs.86671	AV648638	9869652	602079785F2 cDNA, 5' end /clone=IMAGE:4254068 /clone_end=5'	-1	ATATCATATTATTTGATGCCATTAGGC GGCCCTGGATACCAATTCTAAGT
5547	Table 3A	Hs.343475	AV648670	9869684	601556208T1 cDNA, 3' end /clone=IMAGE:3826392 /clone_end=3'	-1	GCCACCAGACAGAAGGACAGAGTT TCTGATTATAAACATGATGCTGGG
5548	Table 3A	Hs.2730	AV650434	9871448	heterogeneous nuclear ribonucleoprotein L (HNRPL), mRNA /cds=(28,1704)	-1	TGTTGGTAGGCAATGTGCAGAGGC GAGCCGCTGAAGTATGGTCTGAG
5549	Table 3A	Hs.312582	AV651615	9872629	601439711F1 cDNA, 5' end /clone=IMAGE:3924482 /clone_end=5'	-1	GGCTGCTGTTGACTGAAATTCTATC CTCAAATTACTCTAGACTGAAGCT
5550	Table 3A	Hs.5897	AV653169	9874183	cDNA FLJ13388 fis, clone PLACE1001168 /cds=UNKNOWN	-1	CTTTTTAGTAGGCAAAGGTTCTCTTC CTCCCTCTTTGGTGCAGGGACGC
5551	Table 3A	NA	AV654188	9875202	AV654188 GLC DNA clone GLCDTC01 3', mRNA sequence	-1	GCGTGTATGTGGATGCCATAGGTG TGACTGTAGACTCATTCTCTTC
5552	Table 3A	Hs.38218	AV659358	9880372	602569369F1 cDNA, 5' end /clone=IMAGE:4693744 /clone_end=5'	-1	TGTAAGTTGACTTCAAAGTCTCTG GAAACACTGGACTTAGCTGGTCC
5553	Table 3A	Hs.133333	AV661783	9882797	AV661783 cDNA, 3' end /clone=GLCGXE12 /clone_end=3'	-1	GAAGCGTGGCAGAGAACTATGGATC AGGCAGCCCCCTCATCTTACCAT
5554	Table 3A	Hs.85844	AV700210	10302181	neurotrophic tyrosine kinase, receptor, type 1 (NTRK1), mRNA /cds=(0,2390)	-1	TTGGTCCAAACTCTGGAGCCTTGTGG GAGAACATAGGGCATAACGTGTTT
5555	Table 3A	Hs.285173	AV700298	10302269	602632207F1 cDNA, 5' end /clone=IMAGE:4777537 /clone_end=5'	-1	CCCTCTTAGTAAAGAGACATCTCT ACAGTAACCACAGAGAAGAAGTGG
5556	Table 3A	Hs.238730	AV700542	10302513	hypothetical protein MGC10823 (MGC10823), mRNA /cds=(63,1235)	-1	TGGACATAACCTGGTCAGAACAGAA ACTTTGAAGCTACAGAACAAAGC
5557	Table 3A	Hs.284674	AV700636	10302607	AV700636 cDNA, 3' end /clone=GKBAGH12 /clone_end=3'	-1	CGGCTCAATAAACCTTACCGGATT TTTGGGGTTATGCCACACCCCTG
5558	Table 3A	Hs.240077	AW002624	5849540	wu60d10.x1 cDNA, 3' end /clone=IMAGE:2524435 /clone_end=3'	-1	GGACCACTAGTACTCCAGAACATAA TATAAAGCATGCCTGAAATGC
5559	Table 3A	Hs.301704	AW002985	5849991	eomesodermin (Xenopus laevis) homolog (EOMES), mRNA /cds=(0,2080)	-1	AACAAGCCATGTTGCCCTAGTCAG GATTGCCCACTTGAGACTTGCTA
5560	Table 3A	NA	AW004905	5853768	wz82d03.x1 NCI_CGAP_Gas4 cDNA clone IMAGE:2565317 3' similar to SW:ATP6_HUMAN P00846 ATP SYNTHASE A	-1	TCTACTGACTATCCTAGAAATCGCTG TCGCCTAAATCCAAGCCTACGTTT
5561	Table 3A	Hs.173280	AW005376	5854154	wz94a12.x1 cDNA, 3' end /clone=IMAGE:2505598 /clone_end=3'	-1	GAGAAACTCCGTGCATGAAGGTTTC CTCCCTGACTCCGCAGCAGCGGCC
5562	Table 3A	Hs.233560	AW006045	5854823	wz81b09.x1 cDNA, 3' end /clone=IMAGE:2565209 /clone_end=3'	-1	CCAAGTAGGTTAACTCTGGTATGG TCTCGTGTTCATTGTTGTGCA
5563	Table 3A	Hs.159643	AW006352	5855130	wt04d12.x1 cDNA, 3' end /clone=IMAGE:2506487 /clone_end=3'	-1	GTTCCCACGGAGCTGACTTCTCCGG GTTGCCCTGCCCCATACATTAACCC
5564	Table 3A	Hs.231987	AW006867	5855645	602320903F1 cDNA, 5' end /clone=IMAGE:4424065 /clone_end=5'	-1	CCGTAACCTCGACAAACGCAGAACCTT CTTGAGGTTCTCTCTAAGGA
5565	db mining	Hs.157118	AW009081	5857859	ws76g10.x1 cDNA, 3' end /clone=IMAGE:2503938 /clone_end=3'	-1	TCTGGACCCCTGCTGGGTTCAAGCA TTGGTGGAGGTAAGTAGTATTCTC
5566	Table 3A	Hs.134272	AW009671	5858449	ws85g09.x1 cDNA, 3' end /clone=IMAGE:2504800 /clone_end=3'	-1	GAAGAGGAAGCTCATCGAAGTCCTC CGACAGAGTGGCCGTATGCCCG
5567	db mining	Hs.131887	AW009730	5858508	602415255F1 cDNA, 5' end /clone=IMAGE:4523725 /clone_end=5'	-1	AGTGTGTATTCTGATGTTATTGGCT CATGTGGACAGAAATGTACAGGG
5568	Table 3A	Hs.232000	AW016002	5864759	UI-H-Blo-abh-h-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2712035 /clone_end=3'	-1	AGATGAGGCTGCTGAGAGATTCACT AATTAGGATGGACAGTCAGCTACT
5569	Table 3A	Hs.233261	AW026667	5880120	wv15d09.x1 cDNA, 3' end /clone=IMAGE:2529617 /clone_end=3'	-1	TGGGCTTGGGGTTCAAGTTGTACCC TTTGGAGACTTATTAATGAAACC
5570	Table 3A	Hs.101340	AW026713	5880166	EST380762 cDNA	-1	CAGTGGTTCTGAGAGAACCTAGTT CAAAGGACTGCCCGCCAAACCCC
5571	Table 3A	NA	AW027160	5885916	wi72b08.x1 Soares_thymus_NHFTh cDNA clone IMAGE:2512983 3' similar to contains Alu repetitive elem	-1	ACCGCCAAAGCCAATCATCCACCTTC AGTACTTACCTAACCAATCTCCCA

Table 8

5572	Table 3A	Hs.233564	AW027530	5886286	wv74c06.x1 cDNA, 3' end /clone=IMAGE:2535274 /clone_end=3'	-1	CAGGATGTATTGACAGGGTGGCCTT TGTGATTCCTCCGGTGGTGGCAGC
5573	Table 3A	Hs.311783	AW043857	5904386	wy81g04.x1 cDNA, 3' end /clone=IMAGE:2554998 /clone_end=3'	-1	GCCATTCATTTGCTGTGGTTAGA CTTCCAGGAGGCTGTTAGCTCA
5574	Table 3A	Hs.277672	AW050975	5913245	wz25f04.x1 cDNA, 3' end /clone=IMAGE:2559103 /clone_end=3'	-1	CCTTTGTAAAAGTCACCTGTGACTG TCAGGGGTATGCTATGGGCCTTT
5575	db mining	Hs.279066	AW063114	8887051	TN0103 cDNA, 3' end /clone_end=3'	-1	GATCCACTTTGGGGTCGGCGGCAG ATTATTCGCTGGTAGAGCCGGATG
5576	db mining	Hs.279082	AW063120	8887169	TN0257 cDNA, 3' end /clone_end=3'	-1	AATAAGGGACTCATTCAATTGCAGC AAATGTTGTTTATTGGCTTGC
5577	db mining	Hs.279083	AW063153	8887202	TN0786 cDNA, 3' end /clone_end=3'	-1	CTCATGGCTCCAGGCCAGGACTCCA TCAGCGCCACGGCTTATCCGAAC
5578	db mining	Hs.279127	AW063155	8887204	DP1003 cDNA, 3' end /clone_end=3'	-1	TTGATGCTCATCATCTGCTGAGGTG ATTGATGCCAGGTTGACGACCAT
5579	db mining	Hs.279104	AW063156	8887205	TN0974 cDNA, 3' end /clone_end=3'	-1	TCCCTGGATAAGGTCACAAACCTGT AACACATGACCCCTAGAGCCCTT
5580	db mining	Hs.279085	AW063158	8887207	TN0311 cDNA, 3' end /clone_end=3'	-1	CCCGCGACTTCACCACCCGCTATCT GGGCACCAAAGACTATATCTAGAT
5581	db mining	Hs.279086	AW063159	8887208	TN0312 cDNA, 3' end /clone_end=3'	-1	CGAACATAGTCTCGACAAGTCCCAA CCCTCCCACCTCGGTGATCAGCT
5582	db mining	Hs.279092	AW063191	8887240	TN0359 cDNA, 3' end /clone_end=3'	-1	CGTCGGGTACCTCGCCGATAAAATC GCTGATGGCTGTCGATCCTGAG
5583	db mining	Hs.279093	AW063196	8887245	TN0360 cDNA, 3' end /clone_end=3'	-1	ATCTTATCCCTCTGTTACTCAATGTGA GTGCATACTTACATTGCCACT
5584	db mining	Hs.279102	AW063210	8887259	TN0377 cDNA, 3' end /clone_end=3'	-1	GGTCCTTGAAGATGACGCCGATGAT CGAGGTCTCTGCCGTAGGCAGATG
5585	db mining	Hs.279067	AW063230	8887055	TN0107 cDNA, 3' end /clone_end=3'	-1	ATGATGAAGCTGCTGTCCAACCCCTT CGCTGCACTTCTGCTGGTGTG
5586	db mining	Hs.279069	AW063239	8887064	TN0018 cDNA, 3' end /clone_end=3'	-1	TCCCTGCCAGAGCCTTCGGGTTCTAC GATTGATCGACCGACGCTGGTGTG
5587	db mining	Hs.279070	AW063242	8887057	TN0138 cDNA, 3' end /clone_end=3'	-1	TGCAACATGGGAGCAGCTCCGTTCAAG ATGGCTAAAGACTAGCGGATTGGG
5588	db mining	Hs.279071	AW063246	8887071	TN0358 cDNA, 3' end /clone_end=3'	-1	AGTGATAGAGACCAAGACTGCTTT TAATTGGTGGGGAGGGGGTGG
5589	db mining	Hs.279072	AW063252	8887077	TN0149 cDNA, 3' end /clone_end=3'	-1	CGGGTCACTCATGTTGGCTACTAAC CTTTCTGCGCCGGGATTCTAG
5590	db mining	Hs.279087	AW063267	8887092	TN0331 cDNA, 3' end /clone_end=3'	-1	CTTGCTCTGATGCCCTCTCTG CAAGGGAGAGCTCTGGACCTCA
5591	db mining	Hs.279073	AW063271	8887096	TN0156 cDNA, 3' end /clone_end=3'	-1	CTGTTTGACATCAGGCCATCTGA CAGCTTATCCGCTATGACTGTT
5592	db mining	Hs.279074	AW063274	8887099	TN0792 cDNA, 3' end /clone_end=3'	-1	CACGAAGCCTTCGATCAGTTGCAGCA CGCGGCCAGAGCGGTCGATAGAAC
5593	db mining	Hs.279122	AW063299	8887124	TN0185 cDNA, 3' end /clone_end=3'	-1	CATTTCGCATCTGCAGCATTGGG TATTGACATGATCCCCAGTGGAGC
5594	db mining	Hs.279076	AW063319	8887144	TN0230 cDNA, 3' end /clone_end=3'	-1	CACCAAGCTGGTCAACATCCAGGCG AATGGCTATTACGTGGATGAGATCA
5595	db mining	Hs.279078	AW063325	8887150	TN0236 cDNA, 3' end /clone_end=3'	-1	TTGCTGATACGGGCTTGTATCATGTT TTCAACGATGTTTCCGGCTTGGC
5596	db mining	Hs.279079	AW063327	8887152	TN0238 cDNA, 3' end /clone_end=3'	-1	CCTCGACAAACTAAATGTTGATTGA ATTGGCTGTTATCATCTGATCAC
5597	db mining	Hs.302423	AW063352	8887289	TN0725 cDNA, 3' end /clone_end=3'	-1	GTTCAGATCGGGCCCGCTCCCGG GGTACCTATAGCGGAATCGAATTTC
5598	db mining	Hs.279095	AW063358	8887295	TN0979 cDNA, 3' end /clone_end=3'	-1	GAAAACAGAAATGATGCTCGGCACAT TCTCGTCCAGCACCTCGGCAACCG
5599	db mining	Hs.279096	AW063371	8887308	TN0746 cDNA, 3' end /clone_end=3'	-1	AACTGTATTGATCACCGTGGCCTG ATGGTGTAGCAGTCGCTTGTTC
5600	db mining	Hs.279097	AW063372	8887309	TN1085 cDNA, 3' end /clone_end=3'	-1	AGTTGACATATAACCCACTTACATAC ATTCCAAATTGCGAGATGAGTGA
5601	db mining	Hs.279075	AW063428	8887365	TN0121 cDNA, 3' end /clone_end=3'	-1	ATATCGTACCGAGAAACTAGTCGGA TATCTGACCGAGGTATGGCGTTTGG
5602	db mining	Hs.279099	AW063436	8887373	TN0922 cDNA, 3' end /clone_end=3'	-1	GTGGATGACCTGATCCAGGTGGCC TGATCGGGCTGACTGATGAGCTGTC
5603	db mining	Hs.279100	AW063458	8887395	TN0949 cDNA, 3' end /clone_end=3'	-1	ATGATGACAGATGCTCTGGCACCGT GTGGAGTTGAGGATGCGACATT
5604	db mining	Hs.279103	AW063469	8887406	TN0981 cDNA, 3' end /clone_end=3'	-1	GATCTGGGACGCATGGCCGAAGCTG AAAAGCTGGCTGAGAACCTCGA
5605	db mining	Hs.279101	AW063474	8887411	TN0354 cDNA, 3' end /clone_end=3'	-1	AACATGGCAATATTATGGTCTCAAT ACTGTCACTGGCAAGGTTGGTGT
5606	db mining	Hs.279821	AW063497	8887434	TN0113 cDNA, 3' end /clone_end=3'	-1	GAGGCAGAGGTGAGCGAGTCAGG CTCTCTCGAACGTTGCACCCGACG
5607	db mining	Hs.279805	AW063509	8887446	TN1012 cDNA, 3' end /clone_end=3'	-1	GTCCCACACGTTGGCCCTGACTCT GCTGTGTTGACGAGGACAACTCG
5608	db mining	Hs.279089	AW063534	8887471	TN1054 cDNA, 3' end /clone_end=3'	-1	CATGACGTGTCGACGACCCAA AGATCACGTAATCAGCCCTGGTGA
5609	db mining	Hs.279080	AW063546	8887483	TN0243 cDNA, 3' end /clone_end=3'	-1	TAGGCTATAGAGATGTTGAGGGATT TATTAGTACACCTCTAGTCATGCC
5610	db mining	Hs.279108	AW063552	8887489	TN1055 cDNA, 3' end /clone_end=3'	-1	GGCTGCCGGATGTTAGGTCTCCC ATGTTGTGAAGTAACGGTGCTCCAC

Table 8

5611	db mining	Hs.279109	AW063556	8887493	TN1059 cDNA, 3' end /clone_end=3'	-1	TGCCCTGTATAGTGTGTAAAAATTA GAATGTTTACCCAAACCATCTGG
5612	db mining	Hs.279110	AW063561	8887498	TN1066 cDNA, 3' end /clone_end=3'	-1	GTCCTTCGAATCGCTCTTAGCTCGT GCGGGCTGTTGTCCCCTTGTTGG
5613	db mining	Hs.279090	AW063572	8887509	TN1079 cDNA, 3' end /clone_end=3'	-1	CTATGCCTGCGCTACAAGCTGGAC CTGTATTGAGCTTCAAGCTACTACC
5614	db mining	Hs.279111	AW063598	8887535	DP0133 cDNA, 3' end /clone_end=3'	-1	TTCGAAGCGACGCTGCGTGCCTGC TCGTCCTAATTGAGCTGATGGATAAGG
5615	db mining	Hs.302424	AW063600	8887537	DP0925 cDNA, 3' end /clone_end=3'	-1	CCTCCCGCTGTCCTCAGTAGCTGT TTCTGTTCCCTGACGCCACTTCT
5616	db mining	Hs.279124	AW063609	8887546	DP0922 cDNA, 3' end /clone_end=3'	-1	CAATGCAGCGGCTGATGAGATCAC CCACGAGATGCAGGACGAAGGCGAG
5617	db mining	Hs.279113	AW063630	8887567	DP0154 cDNA, 3' end /clone_end=3'	-1	TCATTCAGCTGAGTAGGAGGAAAGA GGACAGGTTGGAGAGTTGGTT
5618	db mining	Hs.279114	AW063635	8887572	DP0774 cDNA, 3' end /clone_end=3'	-1	TAATTGCGCTGAAAGCACGAATCTC GAAATGCGTCACCTTCGATTGAC
5619	db mining	Hs.279125	AW063652	8887589	DP0189 cDNA, 3' end /clone_end=3'	-1	AAATGTTGGTACAAGTACCAAGCAG AACTGAGCTGTGTTCTGGAGCCT
5620	db mining	Hs.279116	AW063678	8887615	DP0229 cDNA, 3' end /clone_end=3'	-1	GTTCATCGCTCGCGTGCAGAAGT AAGGGCTAGGCCATGACTCGTTCG
5621	db mining	Hs.279117	AW063709	8887646	DP0336 cDNA, 3' end /clone_end=3'	-1	CTCTGGCAGCCCTGCTCTGTG TCAGCATCGTCCCGTGCCTGGTGG
5622	db mining	Hs.279118	AW063718	8887655	DP0314 cDNA, 3' end /clone_end=3'	-1	GTGCTCGCTGAGCTGGTCCAGAAAT CCGTCGACTGAGCCGATGGCGCG
5623	db mining	Hs.279119	AW063746	8887683	DP0347 cDNA, 3' end /clone_end=3'	-1	CATGAACAAGGGCCGGATCATCTG ATGCCAACACACTGAGCTCCGTG
5624	db mining	Hs.279120	AW063778	8887715	DP0954 cDNA, 3' end /clone_end=3'	-1	CACCCGTTGTAGGCGACGAGCTGA ACGAAAACGTGTCGGACGGCTGTGA
5625	db mining	Hs.279121	AW063780	8887717	DP0388 cDNA, 3' end /clone_end=3'	-1	CATATGCGGCTGTGCCATAGCCGGA TGTCTTCGCGCTGCCTACCCCCG
5626	db mining	Hs.279123	AW063833	8887770	DP0756 cDNA, 3' end /clone_end=3'	-1	TTCTTCCGTCGGCATCGGAATGCG AAACTCGTACTTCGTTAGAAACTC
5627	db mining	Hs.279138	AW063909	8887846	SP0953 cDNA, 3' end /clone_end=3'	-1	GCGAGGGGCTTTACACTCCATGGC CGCAGCGATGACCGGTCACCTG
5628	db mining	Hs.279126	AW063951	8887888	DP0986 cDNA, 3' end /clone_end=3'	-1	CGCCGACCAAGCTTACCGACTTCG CCGATCTACTCGGACGAAGAAGGC
5629	db mining	Hs.279174	AW063977	8887914	DP1019 cDNA, 3' end /clone_end=3'	-1	GGTAGTGCAGTGCCTGAAATGACGGT CCGTCATCATCGGGTCGGAGTAAG
5630	db mining	Hs.279128	AW064020	8887957	DP1073 cDNA, 3' end /clone_end=3'	-1	TTCAGGACTCGTTACGTAGGCAAC GCTGTTAAAGTCCCAAGGGATT
5631	db mining	Hs.279130	AW064046	8887983	SP0153 cDNA, 3' end /clone_end=3'	-1	CTCTTACCCGGAAAACAGGTTGGGA GATGACACGAGAAAAATCATACGC
5632	db mining	Hs.279084	AW064052	8887989	SP0159 cDNA, 3' end /clone_end=3'	-1	CTTGGATATATCGAGAAAGGCCAGG GCCTGAACAAGGAAGCTTCAGG
5633	db mining	Hs.279825	AW064053	8887990	SP0992 cDNA, 3' end /clone_end=3'	-1	AAGGCTGGTCAAGAATCTTGAGACG GAATTGACAGTCTGGCGTGTACCTC
5634	db mining	Hs.279131	AW064060	8887997	SP0636 cDNA, 3' end /clone_end=3'	-1	GATGATTCTGGGGTGACATCGGCG CTGAGCACCATCACCGGAACATAAG
5635	db mining	Hs.279135	AW064084	8888021	SP0612 cDNA, 3' end /clone_end=3'	-1	CTGAGATCACCTGAACACCGACAAG GACGAGATCGCAGTCTGCAACCTG
5636	db mining	Hs.279136	AW064098	8888035	SP0575 cDNA, 3' end /clone_end=3'	-1	CTGAAGGCTTGGCGACAACTGGT CTATCCGTTGAATTGGCGAGAAC
5637	db mining	Hs.302426	AW064100	8888037	SP0684 cDNA, 3' end /clone_end=3'	-1	TCTTGTGCCAGCACGTCTGCTGATA GCCATGAATCGCGTCCCCCTTGTG
5638	db mining	Hs.279175	AW064121	8888058	SP0554 cDNA, 3' end /clone_end=3'	-1	GAACCTCTCAAGGAAATAGTCACCG CCTGCTGTTGGACGCTGCCAGTT
5639	db mining	Hs.279139	AW064129	8888066	SP0696 cDNA, 3' end /clone_end=3'	-1	GTGACCTCGGGGTCCTGCGAAGACG GGGTGCGGCTTGTGAGACGAC
5640	db mining	Hs.279140	AW064136	8888073	SP0570 cDNA, 3' end /clone_end=3'	-1	GTGTCGGGCTTATGTGCCCCAAC CATCGGCACTGGCATCATCGATCC
5641	db mining	Hs.279106	AW064157	8888094	TN1014 cDNA, 3' end /clone_end=3'	-1	AGGTTGATTCCCACTTCTCGGGAGG TTCTGGCACCTTCTGCGCTTGAG
5642	db mining	Hs.279141	AW064160	8888097	SP0594 cDNA, 3' end /clone_end=3'	-1	GTAGCTTCAACGCTTATCTCTGC TCTGAGTGTGTAACCGCGCTGCTC
5643	db mining	Hs.279142	AW064161	8888098	SP0595 cDNA, 3' end /clone_end=3'	-1	TTAAAGTGGTAAGGGAGGTTCTACT CCTGGGAAACATTAAAGTACCTT
5644	db mining	Hs.279143	AW064166	8888103	SP0605 cDNA, 3' end /clone_end=3'	-1	CTTCTCCGACTTCGAGATCTGCCCC TGTCGAGATCGTGGTAGATGATG
5645	db mining	Hs.279144	AW064175	8888112	SP0615 cDNA, 3' end /clone_end=3'	-1	AACTGGATAGAGCACGAGCCTCTAA GCTTGGAGTTGAGCTGAAATCC
5646	db mining	Hs.279824	AW064185	8888122	SP0630 cDNA, 3' end /clone_end=3'	-1	GAAGATCGGCGCAACGAAGACCG TCACTTCACTGGACCAAGAA
5647	Table 3A	NA	AW064187	8888124	(One single EST, artifact?) SP0632 KRIBB Human CD4 intrathymic T-cell cDNA library cDNA 3', mRNA sequence	-1	TGCTTCTGTGACAGATTAGCTTACAT CTTACCCACCTACCGAGAAGAGCT
5648	db mining	Hs.279146	AW064189	8888126	SP0634 cDNA, 3' end /clone_end=3'	-1	AGCTCAAGAGCTTCCGCGACGTAC CAGCAAAGTAACGCTGACGAATGC
5649	db mining	Hs.279145	AW064194	8888131	SP0633 cDNA, 3' end /clone_end=3'	-1	ATCGAAGACGTGATGCTGAACCTTG GGCGAAGGCCAGAAGGAAGGCAAA

Table 8

5650	db mining	Hs.279147	AW064201	8888138	SP0650 cDNA, 3' end /clone_end=3'	-1	CGATACCCCTCACTAGACCTCGGATCG AAATAAATCAGAGCGATCACATCG
5651	db mining	Hs.279132	AW064208	8888145	SP0658 cDNA, 3' end /clone_end=3'	-1	GGGGTACACACCCCCACAAGCTTC CTCGCGCTTCATCAGCGTTACACC
5652	db mining	Hs.279148	AW064218	8888155	SP0732 cDNA, 3' end /clone_end=3'	-1	GATCTTGGTGAGAACGCTGGCATGT AGAAGACCTCGCCCTGGGACACTA
5653	db mining	Hs.279826	AW064223	8888160	SP0676 cDNA, 3' end /clone_end=3'	-1	ATTTTATGCCAGCTACGTGGCATT GGTCAGGACGACCTGAAGGGAAAT
5654	db mining	Hs.279149	AW064250	8888187	SP1013 cDNA, 3' end /clone_end=3'	-1	TGATGCGGAGAGCGAGGTAGATCCC GGCGGAGTTTCGTCGATGGAAAG
5655	db mining	Hs.279150	AW064255	8888192	SP0105 cDNA, 3' end /clone_end=3'	-1	GTACACTTCTGGATCTGATCCAGA GGTAACGAGCGAGAGTGGTGTAC
5656	db mining	Hs.279134	AW064258	8888195	SP0717 cDNA, 3' end /clone_end=3'	-1	GTGACTTCATGCTCGGGGTTGAGCTT GGCGTCCACCCACCTTTTCCCAC
5657	db mining	Hs.279151	AW064272	8888209	SP0130 cDNA, 3' end /clone_end=3'	-1	CCGGTGTCTTGATCAGCTTCAGCAG TGGCTTGACGTAGATGCGGGTCG
5658	db mining	Hs.302427	AW064275	8888212	SP1065 cDNA, 3' end /clone_end=3'	-1	CATCAGTGTTCTCTGCTGGGACTG TTGCATGTTGCTGATCACGGTTG
5659	db mining	Hs.279153	AW064284	8888221	SP0755 cDNA, 3' end /clone_end=3'	-1	GGGAGGCGAAACATAGCTTCCATTGT GTCTTTCTCCTTATGCGTCTTC
5660	db mining	Hs.279156	AW064319	8888256	SP1055 cDNA, 3' end /clone_end=3'	-1	AATGAGACCCGCCGTCCCTGGAGAT GAAGATGTCGTCGACTCCGTCAC
5661	db mining	Hs.279157	AW064320	8888257	SP1045 cDNA, 3' end /clone_end=3'	-1	CGGATGTTGTCGTTCCAGAACGAAG GATCGGCCTTGGGCTGGATTTC
5662	db mining	Hs.279154	AW064343	8888280	SP0916 cDNA, 3' end /clone_end=3'	-1	GGCACCGACTTGGGCTGAGAGGAG CGCAGGTATCAATATAGAATCGG
5663	db mining	Hs.279159	AW064348	8888285	SP1044 cDNA, 3' end /clone_end=3'	-1	CCATGCTGAACCTGGCCAGGTCTTG ACCGCGGTGTTTCCGACAGCACC
5664	db mining	Hs.279161	AW064375	8888312	SP0115 cDNA, 3' end /clone_end=3'	-1	CGCGATGATCTCGCTCTCGCATG GGCATGCGCTATTCTCGACATGG
5665	db mining	Hs.279162	AW064377	8888314	SP1066 cDNA, 3' end /clone_end=3'	-1	GCCCCATTGACCGTATCGCGTATCTT GCTGGCATTTCTAAGAAAATACCG
5666	db mining	Hs.279163	AW064378	8888315	SP0966 cDNA, 3' end /clone_end=3'	-1	TGAACACGGGAAAGGCCAGGAAGAT CTCCGGTTCCACGTCAAATTGTAC
5667	db mining	Hs.279168	AW064424	8888361	SP1056 cDNA, 3' end /clone_end=3'	-1	CAAGAATGACGGAAAAATCCGTGAGC ACAAGGCAAAGGCTTGCCGTG
5668	db mining	Hs.279165	AW064433	8888370	SP1030 cDNA, 3' end /clone_end=3'	-1	GACTTGATCACAAACCGATCCGTAAC GACGTATTGGACCCACTCGAACAA
5669	db mining	Hs.279166	AW064445	8888382	SP1042 cDNA, 3' end /clone_end=3'	-1	CTTCTCGCGTAACCTTCCGCCAG CACGTACGACGTAGGTGTTGT
5670	db mining	Hs.279823	AW064450	8888387	SP1048 cDNA, 3' end /clone_end=3'	-1	TCGACTACGACTTCAACTTCCCCAAA CGGCTGGAGAAGCGAGCTTGAGG
5671	db mining	Hs.279167	AW064452	8888389	SP1069 cDNA, 3' end /clone_end=3'	-1	AAAGTTGATCAGATCACGGGCCACGC CTGCAACCAGAGGCTTGTATCGTC
5672	db mining	Hs.279169	AW064468	8888405	SP1067 cDNA, 3' end /clone_end=3'	-1	TGATCTGATTGTGAGGGAGTTGGAGA AGGTGGTATAGAAGCTGAAAGGGT
5673	db mining	Hs.279155	AW064473	8888410	SP1072 cDNA, 3' end /clone_end=3'	-1	CTTCATGCTCGAGAAGAAAATGCTC GTGCTCCGACGCCACCATCG
5674	db mining	Hs.279170	AW064478	8888415	SP1080 cDNA, 3' end /clone_end=3'	-1	CAGATGGTCACGAGACGCTTGCCG TGATGTCCTCCGTCAGCGTGCAGAG
5675	db mining	Hs.279171	AW064479	8888416	SP0147 cDNA, 3' end /clone_end=3'	-1	TGATGGATTGGAAAGTGTATTCTG TTTACTCTCCCTGCTCTGCTCA
5676	db mining	Hs.279158	AW064487	8888424	SP1087 cDNA, 3' end /clone_end=3'	-1	TTGAAACGGGTATAGCCACCAAGGCAT TGGCTGCAAAGTCGGGCAAAACT
5677	db mining	Hs.330544	AW064490	8888427	SP1090 cDNA, 3' end /clone_end=3'	-1	ACTGTGATTGATGAGTATCTGATGC CTATAACATCTGTTAGGAGGCTACA
5678	db mining	Hs.279160	AW067725	8888472	SP0110 cDNA, 3' end /clone_end=3'	-1	GTACGAAGGTGGCGATGATGCCCTC GATCACCTGGGGATTCTCGCCG
5679	db mining	Hs.279129	AW067742	8888489	SP0150 cDNA, 3' end /clone_end=3'	-1	CGACCTTCGGCGTTCCGCTCCGGAA CCCGTGAAGGCCTTCTACTTG
5680	db mining	Hs.279133	AW067752	8888499	SP0141 cDNA, 3' end /clone_end=3'	-1	TTTCGCTGGCAACATAATTACCAAGAC TCACATCGAACGAAGCTCGGTTCC
5681	db mining	Hs.279154	AW067760	8888507	SP0122 cDNA, 3' end /clone_end=3'	-1	TGTTCTGTTGCCCCATCTTGTGAGGAA CATCTCGCTTCCAGTTCCGCTG
5682	Table 3A	Hs.89433	AW071894	6026892	ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 1, mRNA /cds=(196,4791)	-1	TTTGGGGATCCTTTGTAATGACTT ACACTGGAAATGCGAACATTGCA
5683	Table 3A	Hs.299581	AW073707	6028705	xb01h03.x1 cDNA, 3' end /clone=IMAGE:2575051 /clone_end=3'	-1	GGACAAGGGGCACCCGGATTATATT CCACCAATCTTAATCTAAACCC
5684	db mining	Hs.243286	AW075809	6030807	xa85g05.x1 cDNA, 3' end /clone=IMAGE:2573624 /clone_end=3'	-1	TGGAGCTTATTTGGAGAACACTGTCAC CATTTTATCCAGTTGGCAATT
5685	db mining	Hs.277714	AW075814	6030812	xa85h03.x1 cDNA, 3' end /clone=IMAGE:2573621 /clone_end=3'	-1	ATTATGGGTAAAGGCTTGGGCTGTT CCACATGTTAACCAATGGCCTCA
5686	db mining	Hs.244048	AW075894	6030892	xa81c04.x1 cDNA, 3' end /clone=IMAGE:2573190 /clone_end=3'	-1	GGGAGGGCCAAGAAAATTTTCCC GTTCAAATTATGTTCCCCAAAAA

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5687	db mining	Hs.329433	AW075905	6030903	xa81d05.x1 cDNA, 3' end /clone=IMAGE:2573193 /clone_end=3'	-1	TTACCCCAATGCTTGGCCCGGTGG CCAGTTGAAATTGGTTGATT
5688	db mining	Hs.329434	AW075921	6030919	xa81f04.x1 cDNA, 3' end /clone=IMAGE:2573215 /clone_end=3'	-1	CCCCCTTGGCAGGTTAATTGGTGT TAAGGAACCCCTCAGGGTGGGGGG
5689	db mining	NA	AW075929	6030927	xa81g05.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2573240 3', mRNA sequence	-1	CCCCCCAGTTTAATGTTAGGGGAA GGGATTTAACCCCTTATTAAAAAA
5690	db mining	Hs.265634	AW075948	6030946	xa82b03.x1 cDNA, 3' end /clone=IMAGE:2573261 /clone_end=3'	-1	CTATCACCCCTGATATGAAATTCCAG AATTTCGTGATACACATGGCC
5691	db mining	Hs.277716	AW075986	6030984	xa82f05.x1 cDNA, 3' end /clone=IMAGE:2573313 /clone_end=3'	-1	ACTCCGGGCCTTAATGGATTGGCT GTCCTCAAGAATGGTAATTATGAA
5692	db mining	Hs.241982	AW076004	6031002	xa82h04.x1 cDNA, 3' end /clone=IMAGE:2573335 /clone_end=3'	-1	ACGTGGTTTCAGTCCTAGCACCGTG GTATTGACATGACATCAGTTGCAA
5693	db mining	Hs.257711	AW076027	6031025	he31c12.x1 cDNA, 3' end /clone=IMAGE:2920630 /clone_end=3'	-1	CACAACTTGCTGTTCACGTCTTGGG GTGTTTCCATTCTTAATAGATGG
5694	db mining	Hs.277717	AW076038	6031036	xa83d08.x1 cDNA, 3' end /clone=IMAGE:2573391 /clone_end=3'	-1	AAACCCGTCTCCATTATAATTACCTT TCAAAAGGGCAAGTCAAAAGTTG
5695	db mining	Hs.241983	AW076068	6031066	xa84a02.x1 cDNA, 3' end /clone=IMAGE:2573450 /clone_end=3'	-1	AAACAGCACAACATGAGTGTTCCTA CCACATCAATTAAATGAAGACAC
5696	db mining	Hs.277718	AW076075	6031073	xa84a10.x1 cDNA, 3' end /clone=IMAGE:2573466 /clone_end=3'	-1	CGGAATCGGGTTTCCATTGGACCCCA AAAATTCCCTTGGGCTTCATGA
5697	db mining	Hs.242605	AW076083	6031081	xa84b10.x1 cDNA, 3' end /clone=IMAGE:2573467 /clone_end=3'	-1	TGAGGATAGAACAGCAGCTTTTATT TTTGTGGTAAAGCAAATTGGCA
5698	db mining	Hs.329436	AW076127	6031125	xa84g01.x1 cDNA, 3' end /clone=IMAGE:2573520 /clone_end=3'	-1	GGGGCAAATTCAAGGGACCTCCCC AAAGGGGGTGTTCCTGGATGG
5699	Table 3A	Hs.244816	AW078847	6033999	xb18g07.x1 cDNA, 3' end /clone=IMAGE:2578700 /clone_end=3'	-1	AAACAGGAAGGGGTTTGGGCCCTT TGATCAACTGGAACCTTGGATCAAG
5700	Table 3A	Hs.245616	AW080951	6036103	xc28c10.x1 cDNA, 3' end /clone=IMAGE:2585586 /clone_end=3'	-1	ACTCTTGTCTTTAAAGACCCCTAAT AGCCCTTGTAACTTGATGGCTT
5701	Table 3A	Hs.176498	AW081098	6036250	xc29a12.x1 cDNA, 3' end /clone=IMAGE:2585682 /clone_end=3'	-1	CCGGCTGCCTCCATCCCAGAACAGAGT GCGCAGAGAATTAAATCTAGATATT
5702	Table 3A	NA	AW081232	6036384	xc22e08.x1 NCI_CGAP_Co19 cDNA clone IMAGE:2585030 3' similar to SW:RS1A_HUMAN P39027 40S RIBOSOMAL	-1	GGGATGTAATACATATTTCAAATA AAATGCCCTCATGGGCTTGGGGC
5703	Table 3A	Hs.295945	AW081320	6036472	xc30f12.x1 cDNA, 3' end /clone=IMAGE:2585807 /clone_end=3'	-1	AGAACCCGTATTCATAAAATTAGAC CAAAAAGGAAGGAATCGAACCCCC
5704	Table 3A	Hs.120219	AW081455	6036607	xc31c07.x1 cDNA, 3' end /clone=IMAGE:2585868 /clone_end=3'	-1	AGTTAGTATACAGCCAGAACAGCCAA GCCTCAATTCTGTACCTTGTGTC
5705	Table 3A	Hs.277738	AW082714	6037866	xb61f07.x1 cDNA, 3' end /clone=IMAGE:2580805 /clone_end=3'	-1	CCCTGATCCTCTGTAGGGAACTTCCT TTTCTCTAATCCTAGATCTTCA
5706	db mining	NA	AW088500	6044305	xd10a04.x1 NCI_CGAP_Ov23 cDNA clone IMAGE:2593326 3' similar to SW:BAT3_HUMAN P46379 LARGE PROLINE-	-1	GAGGCATCAGAGGTTCAGGAGAGTT ACAGGCAGCAGGTGGTATAATAT
5707	Table 3A	Hs.243457	AW102836	6073449	xd38h12.x1 cDNA, 3' end /clone=IMAGE:2596103 /clone_end=3'	-1	TTTGTCTTGGGCTGATTGTATC TCTGGAGGCAATTCTTGAA
5708	Table 3A	Hs.341908	AW117189	6085773	xd83f08.x1 cDNA, 3' end /clone=IMAGE:2604231 /clone_end=3'	-1	GCTTGCCTCTGGAGGAGTCAAAG GGGCAGTAAGTATGGGGTGAGAG
5709	Table 3A	Hs.3642	AW130007	6131612	RAB1, member RAS oncogene family (RAB1), mRNA /cds=(50,667)	-1	GCTCCCGAATATTGTAATTGGCC CCCTATGTACCCAAACCCCTGAAA
5710	Table 3A	Hs.248367	AW131768	6133375	MEGF11 protein (MEGF11), mRNA /cds=(159,3068)	-1	AGGAAGTATGAGAGTTCTGAAACCC TGATAGAAACTGGAAGCCTGCAT
5711	Table 3A	Hs.203608	AW131782	6133389	PM0-UT0103_300101-002-f12 cDNA	-1	GACATAGGGTTCACTAGTAGGTGG GCATCTGTTCTAGAAGGCAGTGCC
5712	Table 3A	Hs.335449	AW136717	6140850	UI-H-BI-1-adm-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2717092 /clone_end=3'	-1	TTCTGGCCTTGTACCTAGAAACGC TATTCCTGTATTGGTTCTGGC
5713	Table 3A	Hs.8121	AW137104	6141237	Notch (Drosophila) homolog 2 (NOTCH2), mRNA /cds=(12,7427)	-1	GCTCTGGAAAGAGACAGGAAAGTC TGGATGGAAAAGAACACGATGAGA

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5714	Table 3A	Hs.12035	AW137149	6141282	602122419F1 cDNA, 5' end /clone=IMAGE:4279300 /clone_end=5'	-1	GGGTTACATTTGAGTCTCTGTACCTG CTTGGAAGAAATAAAAATACGTGT
5715	Table 3A	Hs.342003	AW138461	6142779	UI-H-BI1-adg-e-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2716882 /clone_end=3'	-1	CTGGGAATATGAAGCGAACGCCACA CACTAGAACGCCCTGGAGCTGG
5716	Table 3A	Hs.245138	AW139918	6144636	UI-H-BI1-aeo-d-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2719136 /clone_end=3'	-1	GCTGCTTTGCCATCCAGGTTCCA CATCCTAATCTTGCTTTCTTGT
5717	Table 3A	Hs.276718	AW148618	6196514	601473284T1 cDNA, 3' end /clone=IMAGE:3876165 /clone_end=3'	-1	TGAAATGTGGTTGACTATTTCGTAT TGCCCCATCTATTGATGAGGGT
5718	Table 3A	Hs.89104	AW148765	6198661	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	TTGTTTAACAACTCTCTCACATT TTGCCAGTTATTCACTGTAAACCA
5719	Table 3A	Hs.248657	AW150084	6198076	xg36f03.x1 cDNA, 3' end /clone=IMAGE:2629661 /clone_end=3'	-1	ACATAAACTGTCCCTTAGGAAGAAG CCCATGCCGATTTGCCCTTA
5720	Table 3A	NA	AW150085	6198077	xg36f04.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2628663 3' similar to gb:X65018 PULMONARY SURFACTANT-ASSOC	-1	GGACAAAGTGGCATCGGACTATATT CCCACCAATCTAACCTAACATCCC
5721	Table 3A	Hs.265838	AW150944	6198842	xg42e09.x1 cDNA, 3' end /clone=IMAGE:2630248 /clone_end=3'	-1	TATGTCCTTTCTCCTCCCTCCCC ATTCCCTGGCATCATATTGGGAC
5722	Table 3A	Hs.301104	AW151854	6199839	602313002F1 cDNA, 5' end /clone=IMAGE:4422480 /clone_end=5'	-1	CGCTGTCGCCTTAATCCAAGCCTACG TTTTACACTCTAGTAAGCCTCT
5723	Table 3A	Hs.337727	AW161820	6300853	au70h03.x1 cDNA, 3' end /clone=IMAGE:2781653 /clone_end=3'	-1	TGTGGGCTTGGTATAAACCTACTTT GTGATTGCTAAAGCACAGGATGT
5724	Table 3A	Hs.299967	AW166001	6397528	xf43e11.x1 cDNA, 3' end /clone=IMAGE:2620844 /clone_end=3'	-1	CCGCCTGAAACGGGCATTTGTAAAT GGGGTTGACTATTTGTATGTC
5725	Table 3A	Hs.81248	AW166442	6397967	CUG triplet repeat, RNA-binding protein 1 (CUGBP1), mRNA /cds=(137,1585)	-1	ACTGGCAAATGAAGCATACTGGCTTG CAGGGACCTCTGATTCAAGTACA
5726	Table 3A	Hs.169738	AW172306	6438254	xj37a08.x1 cDNA, 3' end /clone=IMAGE:2659382 /clone_end=3'	-1	GAATTGATTTGAGATCTGAGGGCAG ACCCGAACCGAGAAAGCAACTCG
5727	Table 3A	Hs.8991	AW172850	6438798	adaptor-related protein complex 1, gamma 2 subunit (AP1G2), mRNA /cds=(45,2402)	-1	AATGCAACCAGGCTGCCACCTGCACC AGTGGTTGCTACATGGATAAGAAA
5728	Table 3A	Hs.143525	AW173163	6439111	xj84b08.x1 cDNA, 3' end /clone=IMAGE:2663895 /clone_end=3'	-1	TATGATAGGATTCTCCACAGTGGCTT CCGACTCAGGCTCAAATGGACCAA
5729	Table 3A	Hs.38664	AW188135	6462571	IL0-MT0152-061100-501-e04 cDNA	-1	TGCTGTATGGGCAGGGTGTCTTATA TGTGATCAACAGATGTCCAGGAAC
5730	Table 3A	NA	AW188398	6462834	xj98c03.x1 NCI_CGAP_Co18 cDNA clone IMAGE:2665252 3', mRNA sequence	-1	ACCTCCAAGAACATCTGCCCTTGTG AACGTGTTTACCTGTCCACTC
5731	Table 3A	Hs.252989	AW191929	6470628	xj77c10.x1 cDNA, 3' end /clone=IMAGE:2680722 /clone_end=3'	-1	CCTTTGCCCTTAGCCCTGGATAA TCCGGCTGGATGGGGTGAGGG
5732	Table 3A	Hs.203755	AW194379	6473179	xm08h07.x1 cDNA, 3' end /clone=IMAGE:2683645 /clone_end=3'	-1	CCCAAATAAGCTCTGACTTCGGTA CCTATGTACCTGTTACCACTTCA
5733	Table 3A	Hs.253151	AW195119	6474139	xn66b07.x1 cDNA, 3' end /clone=IMAGE:2699413 /clone_end=3'	-1	GCCACATGTCTTACACAGGT GCTTAAATTCAAGCCCAGTCTCA
5734	db mining	Hs.253154	AW195169	6474211	xn66h03.x1 cDNA, 3' end /clone=IMAGE:2699477 /clone_end=3'	-1	CTTGAAGGGCTTTGGTTGGGTTTG GGGTTTTGGGTGGGACTCCAAAG
5735	db mining	Hs.330019	AW195270	6474330	xn67c04.x1 cDNA, 3' end /clone=IMAGE:2699526 /clone_end=3'	-1	GGGGTTTAAAAATTTCGGCCCGGG
5736	db mining	Hs.253167	AW195284	6474352	xn67d09.x1 cDNA, 3' end /clone=IMAGE:2699537 /clone_end=3'	-1	CCCCCTGGGTTTTGGGAATGAGG TAAGGCTTGAATTGGTTGATAT
5737	db mining	Hs.253168	AW195300	6474368	xn67f12.x1 cDNA, 3' end /clone=IMAGE:2699567 /clone_end=3'	-1	ACATGCTTAGAGCTGGAGGCTTGAAA CCATAATCCCAATTAAAGTCTGTC
5738	db mining	Hs.253169	AW195313	6474381	xn67h05.x1 cDNA, 3' end /clone=IMAGE:2699577 /clone_end=3'	-1	TGTTTGCTCAGGAAAAGGAAGAGGG GGAAATTAAAACCTTCCGGTTAGT
5739	Table 3A	Hs.253384	AW204029	6503501	UI-H-BI1-aen-d-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2719899 /clone_end=3'	-1	GCACTGCTCCGCTAGCTGTATGACC TTTGTATGTTCTTCTCCGT
5740	Table 3A	Hs.253502	AW205624	6505098	UI-H-BI1-afn-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2722657 /clone_end=3'	-1	CTTCATCTGGCTGGCACTCCAC GCACATAATCGTCACTCTGGAGGA

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5741	Table 3A	Hs.330058	AW206977	6506473	Ui-H-BI1-afs-h-11-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2723180 /clone_end=3'	-1	GCGGGAAAGTGAAGCGGAGGGCTGGG ACAAGGGAACTTACTGCTAAAAAA
5742	Table 3A	Hs.157315	AW207701	6507197	Ui-H-BI2-aga-e-03-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2724172 /clone_end=3'	-1	AGTGGTGTGGTGGCAATAGAAAAG AAAAGATCAGGATGAGAAATTGCTT
5743	db mining	NA	AW236186	6568575	xn70e07.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2699844 3', mRNA sequence	-1	CCAAGGGCCTTTGGGTTGTTCCCT ATAACCTCAGTATTGAAATTAGT
5744	db mining	NA	AW236203	6568592	xn70h07.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2699869 3', mRNA sequence	-1	CATAAAGGGCATTGCCCTAGCCGG TCCGGCCTTTCCAGTCATCTG
5745	db mining	Hs.330063	AW236208	6568597	xn71a06.x1 cDNA, 3' end /clone=IMAGE:2699890 /clone_end=3'	-1	AGGTTTAAGAAATTCCCCCTAAATCTT GTTTGGTGGGGATGAAAAGT
5746	db mining	Hs.253747	AW236252	6568641	xn71g08.x1 cDNA, 3' end /clone=IMAGE:2699966 /clone_end=3'	-1	AATTGATCCCATTCTTGCTGAAGTAG ACAGTGCCTCAAGTGGAAATTAA
5747	db mining	Hs.253748	AW236271	6568660	xn72b03.x1 cDNA, 3' end /clone=IMAGE:2699981 /clone_end=3'	-1	CTCCAATGCTGTTATCCGGCTGGGT CCTCACACTCCCCAACATCCCA
5748	db mining	NA	AW236345	6568734	xn73c12.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2700118 3' similar to contains element MER21 repetitive e	-1	AGAATGCGCTATTCCCTCAAGCCC TGCGCTGAATAAAGAAGCCGATT
5749	Table 3A	Hs.253820	AW237483	6569872	xm72e01.x1 cDNA, 3' end /clone=IMAGE:2689752 /clone_end=3'	-1	CTGAGGTCAGTGTGGTTGGAA GGATTATGATATTACAAGCTGAGT
5750	Table 3A	Hs.342342	AW243795	6577635	xo56f02.x1 cDNA, 3' end /clone=IMAGE:2707995 /clone_end=3'	-1	GGTCAATGTTGAAATTGTGGAGC AAACCCCGAGTTTATGCCCTGGT
5751	Table 3A	Hs.250591	AW262077	6638893	xp19e09.x1 cDNA, 3' end /clone=IMAGE:2740840 /clone_end=3'	-1	AGTTGGAAAATTAGAAATGTCACT GTAGGACGTGGAATATGGCGTCGA
5752	db mining	Hs.250591	AW262272	6639088	xp19e09.x1 cDNA, 3' end /clone=IMAGE:2740840 /clone_end=3'	-1	TTCACGTCTAAAGTGTGGTAGACGC GCCCGCGAATTAGTAGTAGTAGG
5753	Table 3A	Hs.277994	AW262728	6639544	xq94a12.x1 cDNA, 3' end /clone=IMAGE:2758270 /clone_end=3'	-1	GGACAAGTGGCATCCGTATTATTT CCCACCATTCCATTCTTAATCCC
5754	db mining	Hs.61345	AW262891	6639707	mRNA for KIAA1154 protein, partial cds /cds=(0,676)	-1	GGTCTGCCCTCAGTCTTACTCATCA GCACACACTGTCAAAATGTTGGA
5755	Table 3A	Hs.5662	AW264291	6641033	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA /cds=(95,1048)	-1	AGATGAATTGAAGCAAAAGTTTCA GTACCAAGCACCAAGGCAGACCCC
5756	Table 3A	Hs.122655	AW274156	6661186	hypothetical protein MGCI4425 (MGCI4425), mRNA /cds=(318,686)	-1	TCACCTCCACCTCTGAGGGAGCAAC GAATACAAAGGTAGACCCCCAAAAG
5757	Table 3A	Hs.250600	AW281304	6697940	Ui-H-BI2-agh-a-02-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2724386 /clone_end=3'	-1	CCCCAGCCAGCACTTCCCTTTCTGC GAGGGTTTCTGTTCTTGATTA
5758	Table 3A	Hs.47325	AW291458	6698021	Ui-H-BI2-agh-c-02-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2724099 /clone_end=3'	-1	AGAAAATTGAAACCCATCGCTCTCC CATCCCACCTCTTACTCCATCCCG
5759	Table 3A	Hs.170381	AW291507	6698143	Ui-H-BI2-aga-g-11-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2723900 /clone_end=3'	-1	CTGTGGCATTCATCACACCACAGCA GAGTCCCTCCAAGAGGGCTG
5760	db mining	Hs.255118	AW292757	6699393	Ui-H-BW0-aj-b-12-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2729423 /clone_end=3'	-1	CCGTGTTAAACCAAAGTTGGGATT TTTCGGGTATTCACTGGAAAGTCAC
5761	Table 3A	Hs.255119	AW292772	6699408	Ui-H-BW0-aj-d-03-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2729501 /clone_end=3'	-1	CGAGAGCCTGAAAGCTTGCAACTA CTGCCTGGAAGATCTGATTCTTG
5762	db mining	Hs.255123	AW292814	6699450	Ui-H-BW0-aj-h-02-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2729691 /clone_end=3'	-1	TGTTTAAAGTGGTTATTCACCC CTTTCACTCCGGTTGGTACCG
5763	db mining	Hs.255129	AW292855	6699491	Ui-H-BW0-aj-d-03-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2729117 /clone_end=3'	-1	TCTTCTCAGTCTCAGCAAGTAGC TTCTTCAGAACTGCCTCCTCCG
5764	db mining	Hs.255544	AW292873	6699509	Ui-H-BW1-ame-e-09-0-Ul.s1 cDNA, 3' end /clone=IMAGE:3069784 /clone_end=3'	-1	GTTTCTGCATCCCAAATGTCTGGG GCATGTGTCCCTCTGCTGACC
5765	db mining	Hs.255134	AW292900	6699536	Ui-H-BW0-ajg-a-05-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2729000 /clone_end=3'	-1	TGTTATGATTCTCAATTCTCAAAG CTCTTCTGGCAGAGGAGACAGAT
5766	db mining	Hs.255135	AW292902	6699538	Ui-H-BW0-ajg-a-07-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2729004 /clone_end=3'	-1	AAATGGGATTACAATTCCCTGACATT GGGCATAAAACATCTGCCATCCT
5767	db mining	Hs.255139	AW292928	6699584	Ui-H-BW0-ajg-d-11-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2729158 /clone_end=3'	-1	TCCTCCCTCCAGAGACCTTGTGTTA CTGCCATTCTGTGGGCTTT
5768	db mining	Hs.255140	AW292941	6699577	Ui-H-BW0-ajg-f-10-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2729250 /clone_end=3'	-1	AGGCATAGCAGTAGAATCTGCAAA AGGAGGCATGGAATGAAATGAACC

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5769	db mining	Hs.255142	AW292980	6699596	UI-H-BW0-aih-a-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2728995 /clone_end=3'	-1	CTGACCCCTCTGCCCTCCACCTGTG CTTCTGCCCTAGGATAACGCTGG
5770	db mining	Hs.147728	AW292989	6699525	RST12623 cDNA	-1	GACCCAAAGAAAAGATCAAGACCGCA TGTAGCAAATGTAGCAAGGAGGCA
5771	db mining	Hs.255152	AW293001	6699537	UI-H-BW0-aih-d-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729159 /clone_end=3'	-1	CTAATTCCCACACTAAAGGTCCAGAA AAATTGATGCCACCTGTAGTTGG
5772	db mining	NA	AW293017	6699653	UI-H-BW0-aih-f-06-0-Ui.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2729243 3', mRNA sequence NCI_CGAP_Sub6 cDNA clone IMAGE:2729356 3', mRNA sequence UI-H-BW0-aih-b-07-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729412 /clone_end=3'	-1	GTAAAGTTCCAACGCAGTGGAAAGGTA AACACGACTGTGGCACCGGAGCC
5773	db mining	NA	AW293143	6699779	UI-H-BW0-aii-a-03-0-Ui.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2729356 3', mRNA sequence UI-H-BW0-aii-b-07-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729412 /clone_end=3'	-1	GAAACTGAATGACCATGGAATGCTGA ATTCCAAAAGAAAAACGTGCGC
5774	db mining	Hs.255172	AW293158	6699794	UI-H-BW0-aii-b-07-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729412 /clone_end=3'	-1	TCTCTCAGGTCGTCCTCAGACTCCAT TCCCTTGTCTTGATCTTCTCT
5775	Table 3A	Hs.166975	AW293159	6699795	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(218,541)	-1	CTCCCACATTCCTCCCGAACGCCA TTTGTTCAAGTGTCTATCCACGC
5776	db mining	Hs.255174	AW293172	6699808	UI-H-BW0-aii-c-10-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729466 /clone_end=3'	-1	GCCCTGCCCTACCCCTGCCCTTA ATTTCGGACTGAATAAGAAT
5777	Table 3A	Hs.255178	AW293267	6699829	UI-H-BW0-aii-e-10-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729562 /clone_end=3'	-1	TGCAGGATAACTTGTCTATGAAAGGA AATGCCAGATTAAACCCCTTCCA
5778	Table 3A	Hs.75354	AW293424	6700060	mRNA for KIAA0219 gene, partial cds /cds=(0,7239)	-1	GCCTTCCCTCGTTCTTCCAGGCA ATAATGACATATTAGTATGCAA
5779	Table 3A	Hs.255200	AW293426	6700062	UI-H-BI2-ahm-b-02-0-Uls1 cDNA, 3' end /done=IMAGE:2727122 /clone_end=3'	-1	CGCCACGGCTCCAATCCCTATATGAG TGAGCAGTAGAATCACATAGGAAT
5780	Table 3A	Hs.10041	AW293461	6700097	602713308F1 cDNA, 5' end /clone=IMAGE:4853616 /clone_end=5'	-1	CCTAGAACTCAGACTTTAACGACAAGC AGGGAGGGAAAGCACTTGAGCACT
5781	db mining	Hs.291317	AW293859	6700495	rx40e10.s1 cDNA, 3' end /clone=IMAGE:1258602 /clone_end=3'	-1	GCACATGCAAAACTCAGATGTGCAA ATAACTGTCCTTAACTACAA
5782	Table 3A	Hs.255249	AW293895	6700531	UI-H-BW0-ain-f-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729995 /clone_end=3'	-1	GGTGCTCAAACGTATTTCTCCCTC CCTCCCTCTTCTTCCAGA
5783	db mining	Hs.255251	AW293922	6700558	UI-H-BW0-alk-a-04-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729382 /clone_end=3'	-1	TTCTTCCACGGGATTCTTAATTCTTA AATAGGACCTCCACACCAGACCT
5784	db mining	Hs.255253	AW293949	6700585	UI-H-BW0-alk-c-10-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729490 /clone_end=3'	-1	TATCCAGCTGACTCTCATGCTGT ACTAGCCTCCAACTCTAACTAA
5785	db mining	Hs.255254	AW293950	6700588	UI-H-BW0-alk-c-11-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729492 /clone_end=3'	-1	TGGACATTGGGGGTCAAACCCCTTTG TTTAAATTTCCTTCCAGGGC
5786	Table 3A	Hs.255255	AW293955	6700591	UI-H-BW0-alk-d-05-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729528 /clone_end=3'	-1	GCTGTGCCACGGTCAGGTGGCTTCC AATCTGTACTCAATTGTTACTGTAC
5787	Table 3A	Hs.190904	AW294083	6700729	UI-H-BI2-ahg-b-05-0-Ui.s1 cDNA, 3' end /done=IMAGE:2726720 /clone_end=3'	-1	TCAGAGATGCTGATGTATATAAGTA GTTCCCTGTCTGGCCTTGGATGT
5788	db mining	Hs.255330	AW294618	6701254	UI-H-BW0-alk-a-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729385 /clone_end=3'	-1	GTATGACTGATGATAGCTGCGAATGA GGAGGAGGAAAGGGAGGCTGGAG
5789	db mining	Hs.255333	AW294644	6701280	UI-H-BW0-alk-c-11-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729493 /clone_end=3'	-1	CCATTGCCCGGTGTTGGTTAAAT TTCCCCAGGCTTAACTAAAGGCC
5790	Table 3A	Hs.255687	AW294654	6701290	UI-H-BW0-alk-d-10-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729539 /clone_end=3'	-1	AGGAAATTAAACATGAGCATGACATG ACCCCAACCTCAAGAAATCCCCA
5791	Table 3A	Hs.255336	AW294681	6701317	UI-H-BW0-alk-g-10-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729683 /clone_end=3'	-1	ATCAGGTCCCCTACAAAATTAGCTAC TTTGGCCTTCCTACAAAATTAGC
5792	db mining	Hs.255337	AW294692	6701328	UI-H-BW0-alk-h-11-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729733 /clone_end=3'	-1	TCATTCTGTTGCTTCTCTGACTGACA GGCAGTAATGACTTCATAAGCT
5793	Table 3A	Hs.255339	AW294695	6701331	UI-H-BW0-alm-a-02-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729738 /clone_end=3'	-1	AGGGCCTGCTTCAGAGTTGTTCCCT AAATAAAACAATGGCTCTCCCCGT
5794	db mining	Hs.255341	AW294697	6701333	UI-H-BW0-aim-a-04-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729742 /clone_end=3'	-1	CCCCCAACTTACATGGAAAAGGGATG GTTGCATTCTGTGTATATGCAT
5795	db mining	Hs.342539	AW294717	6701353	UI-H-BW0-ajl-g-03-0-Ui.s1 cDNA, 3' end /done=IMAGE:2732333 /clone_end=3'	-1	GCAGAGGGAAGAGGAAATGCTTGA AGCCTTGCTAGTTATTTAATTAGTT
5796	db mining	Hs.255347	AW294739	6701375	UI-H-BW0-aim-f-07-0-Ui.s1 cDNA, 3' end /done=IMAGE:2729988 /clone_end=3'	-1	GACATAGTTGCCAAAACAATACTTA ATACTTTCTGGAGGAGGGGCC

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5797	db mining	Hs.255354	AW294769	6701405	UI-H-BW0-aii-g-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729667 /clone_end=3'	-1	ACCCCTTTCTTAATTTCAGGAAAA TGGCAGCTCCTCTTTGCGTC
5798	db mining	NA	AW294812	6701448	UI-H-BI2-ahi-d-06-0-Ui.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2726842 3', mRNA sequence	-1	CCTCCGGTGTCTCGGAAGCACTGAA GGGACATCTGGGACCCCTCACCTG
5799	db mining	Hs.255388	AW295071	6701707	UI-H-BW0-aii-c-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730245 /clone_end=3'	-1	ACTCTTGACCAAATAAATCACTGGAA TAGAGGTTCCAGCATATTCTGAGA
5800	Table 3A	Hs.255389	AW295088	6701724	UI-H-BW0-aii-d-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730305 /clone_end=3'	-1	ATGCTTACACCCCTGGATGAATAAAAGT CTTTATTACACCTCCACCTCCCC
5801	db mining	Hs.255157	AW295376	6702012	UI-H-BI2-ahv-f-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2728085 /clone_end=3'	-1	CTCTTCACAGGTCTATAAGCCCCCTTG AGCGGCAGACTCCTCGCATCCAG
5802	db mining	Hs.330175	AW295597	6702233	UI-H-BW0-aii-a-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729779 /clone_end=3'	-1	CAGCTCGACCTCAGTCCCTTCAGAA ATAAGATGGCGGCTGCCTGACAG
5803	Table 3A	Hs.255446	AW295610	6702248	UI-H-BW0-aii-c-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729861 /clone_end=3'	-1	TTICAACGTGTACCTTCTGGAAA CCATCTCAATAAACACATTTGGT
5804	db mining	Hs.255448	AW295616	6702252	UI-H-BW0-aii-c-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729873 /clone_end=3'	-1	GCTGGACACATGGGTTAAGAGGAGG AAAAGTAGGAAAGGAGGAGGGAAA
5805	db mining	Hs.255449	AW295629	6702265	UI-H-BW1-amu-a-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3071128 /clone_end=3'	-1	GGCTGGGACCAGGGTTTCAAGCC ACCTTTCTGTCTCAGTTCAAGAGA
5806	Table 3A	Hs.255454	AW295664	6702300	UI-H-BW0-aii-g-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730071 /clone_end=3'	-1	CCCACTTTCACACATGACTCACACGA CTGAAGGAAAGAAAGGGCATCCTT
5807	db mining	Hs.255455	AW295669	6702305	UI-H-BW0-aii-h-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730107 /clone_end=3'	-1	AAGAAATTAAAGGAAGGCAAGAGGGTA GGTTGGCCCATGGAAAGTTCCC
5808	db mining	Hs.255457	AW295688	6702324	UI-H-BW0-aiw-b-02-0-Uls1 cDNA, 3' end /clone=IMAGE:2730578 /clone_end=3'	-1	CTGGCAAATTGCGGAAGATGACT GAAATGTAATTGAAATGTAGCTGC
5809	db mining	Hs.255459	AW295711	6702347	UI-H-BW0-aiw-d-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730678 /clone_end=3'	-1	AGCATAAGAGATAACGAAGCTGATGGT AATTAACTGTACCCCTGAAGTG
5810	db mining	Hs.255462	AW295724	6702360	UI-H-BW0-aiw-e-08-0-Uls1 cDNA, 3' end /clone=IMAGE:2730734 /clone_end=3'	-1	AGTGTAGACAATTAGATACTCTTC CTGTCTTCAGGAGCCATCTGGAA
5811	db mining	Hs.255464	AW295731	6702367	UI-H-BW0-aiw-f-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730776 /clone_end=3'	-1	GAAGTGTAAACATGCCAACAGGTTT ATATTAGGTTCAAGAGTTGCA
5812	Table 3A	Hs.156814	AW295965	6702531	KIAA0377 gene product (KIAA0377), mRNA /cds=(126,4346)	-1	CTTCCCAAACCTCATTGTCCTCATCTC ACTGCTTATGTTATTGCTCTTAT
5813	Table 3A	Hs.255492	AW296005	6702641	UI-H-BW0-aii-b-01-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730552 /clone_end=3'	-1	CCACACAGCAGAGAAGTATCAGAAA ACATAGAAACATGTGAAAATGCGC
5814	db mining	Hs.255495	AW296020	6702658	UI-H-BW0-aii-c-07-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730512 /clone_end=3'	-1	AGGTTCAATTCTTCTGAGATGTT TGGTTATAAGATTGAGGATGTT
5815	db mining	Hs.255497	AW296044	6702680	UI-H-BW0-aii-e-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730714 /clone_end=3'	-1	ATACTTAGATGTGCTTGGATCTGGG TGGGAGGCTTGGTTAGAAGTCACG
5816	db mining	Hs.255498	AW296054	6702690	UI-H-BW0-aii-f-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730762 /clone_end=3'	-1	TGGGTCAAGCGTGTCAATTAAATAA GGAATACACTAGCCTTACAACGGA
5817	db mining	Hs.255499	AW296058	6702694	UI-H-BW0-aii-g-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730794 /clone_end=3'	-1	TGTTCATCTTGATGTAATAGAGAAGG AAAGAGAGAGCATCCCTTTCAGT
5818	Table 3A	Hs.255501	AW296063	6702699	UI-H-BW0-aii-g-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730806 /clone_end=3'	-1	ACAGTAACACAATGACGGCAAGCAC AGAGAAGGAAAAGTCAGATCCCC
5819	db mining	Hs.255502	AW296066	6702702	UI-H-BW0-aii-g-11-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730812 /clone_end=3'	-1	ACTTGGAGCTAGAGAGCACCACATCA TATGGAGGAGAAAGTGGTCACTCTA
5820	db mining	Hs.34871	AW296352	6702988	zinc finger homeobox 1B (ZFHXB1B), mRNA /cds=(444,4088)	-1	TGCATGTGTTGTGTACTTGTCTGT TCTGTAAGATTGTCGGTGTACAC
5821	db mining	Hs.255543	AW296373	6703009	UI-H-BW0-aii-h-00-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729874 /clone_end=3'	-1	TTCCTGGCAAGTAAGAAAAGAAAGAA GATGTGAGTTATGAAGCATTGACT
5822	db mining	Hs.255546	AW296398	6703034	UI-H-BW0-aii-f-01-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730000 /clone_end=3'	-1	AAATAGGAATATAATCTGTCCACATC AAAAGAATGGGAAGTCGAAGTGTACA
5823	db mining	Hs.255549	AW296404	6703040	UI-H-BW0-aii-f-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730014 /clone_end=3'	-1	GTTCCAAATGTTCCGCTAATAGTT GTCCCTAAAGCCTTGCCTATTCCCT
5824	db mining	Hs.255552	AW296446	6703082	UI-H-BW0-aii-b-07-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730180 /clone_end=3'	-1	ACAGAGAAGGCTTACGTGGGAA ATTACATTAAGGAAAAGTGGTAC

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5825	Table 3A	Hs.255554	AW296490	6703126	UI-H-BW0-aiq-f-08-0-Uls1 cDNA, 3' end /clone=IMAGE:2730374 /clone_end=3'	-1	CCTTCCTCCTATATCCTGCCTTGAAT AGGGATGTGATACCTTGAGGCCATG
5826	db mining	Hs.255556	AW296504	6703140	UI-H-BW0-aiq-g-12-0-Uls1 cDNA, 3' end /clone=IMAGE:2730430 /clone_end=3'	-1	ATATTGGGTCTCTGTTAAGATTCA TTGCCGTGGTAGGGAGAGTTCA
5827	db mining	Hs.255558	AW296511	6703147	UI-H-BW0-aiq-h-08-0-Uls1 cDNA, 3' end /clone=IMAGE:2730470 /clone_end=3'	-1	TGGATGCCATGATGACACCAATAAGC AACCCACAGATTAGGGAAATACT
5828	Table 3A	Hs.255559	AW296532	6703168	UI-H-BW0-aiq-b-07-0-Uls1 cDNA, 3' end /clone=IMAGE:2730585 /clone_end=3'	-1	GGGGCTGGGAGGCCACCAAAAGGGCC TGCTCTCGGAGAAAATGCTGAATT
5829	Table 3A	Hs.255560	AW296545	6703181	UI-H-BW0-aiq-c-11-0-Uls1 cDNA, 3' end /clone=IMAGE:2730621 /clone_end=3'	-1	AGGCATCTTGAAGTTCATAAAGAC AGAACGTAAGGGTCATTCACTT
5830	db mining	Hs.255561	AW296567	6703203	UI-H-BW0-aiq-f-04-0-Uls1 cDNA, 3' end /clone=IMAGE:2730751 /clone_end=3'	-1	AGCTAAAGCCACGGAACTAATGAGA TTTATGCATGAAAGAACAGGTT
5831	db mining	Hs.255569	AW296695	6703331	UI-H-BW0-aiq-c-06-0-Uls1 cDNA, 3' end /clone=IMAGE:2730635 /clone_end=3'	-1	TGTTCTCTCGAACCTCTGGAGCAC ATCAGCTCTCTGCATAAATCTGTT
5832	db mining	Hs.255572	AW296727	6703363	UI-H-BW0-aiq-f-09-0-Uls1 cDNA, 3' end /clone=IMAGE:2730785 /clone_end=3'	-1	ATCTGGAGGATGGCAGTTGAGAATT AGGACTAAGCCCCTCTCCCTT
5833	Table 3A	Hs.255573	AW296730	6703366	UI-H-BW0-aiq-f-12-0-Uls1 cDNA, 3' end /clone=IMAGE:2730791 /clone_end=3'	-1	CATTAGCTCTAAACATTGGCTA AGGGATTATAGGTGAAGCCTTAA
5834	db mining	Hs.255575	AW296758	6703394	UI-H-BW0-ajb-a-10-0-Uls1 cDNA, 3' end /clone=IMAGE:2730931 /clone_end=3'	-1	GGTAGGATTATCCCTTTCTTCATGTG CAACTGTATAAACTGGCAAAGCA
5835	db mining	Hs.255577	AW296773	6703409	UI-H-BW0-ajb-c-04-0-Uls1 cDNA, 3' end /clone=IMAGE:2731015 /clone_end=3'	-1	AGTCTTATGGGACAGAGCAGCTCTCC AGTCTAGGATGGTAGAAAGATTCTT
5836	Table 3A	Hs.255579	AW296797	6703433	UI-H-BW0-ajb-e-07-0-Uls1 cDNA, 3' end /clone=IMAGE:2731117 /clone_end=3'	-1	GAGTCTGTACCCCTTCTAATAAACT GCTCTGGACACAATGAACCTGTAA
5837	db mining	Hs.255580	AW296802	6703438	UI-H-BW0-ajb-f-02-0-Uls1 cDNA, 3' end /clone=IMAGE:2731155 /clone_end=3'	-1	CCATGGCAAGCCTGGTGGGTTCAT ATTCACTGGATTAGGGATTAAAGG
5838	db mining	Hs.255590	AW296914	6703550	UI-H-BW0-ajc-a-12-0-Uls1 cDNA, 3' end /clone=IMAGE:2731294 /clone_end=3'	-1	CCATTTCTCTGGATCCTCTCTAGTT GTCTTGTGTGGACGCAAGCG
5839	db mining	Hs.255591	AW296947	6703583	UI-H-BW0-ajc-e-05-0-Uls1 cDNA, 3' end /clone=IMAGE:2731472 /clone_end=3'	-1	GATCTTTGCTGACACTGGTTCTCT CTTATTTGCCCGCCAATAAA
5840	db mining	Hs.255598	AW297024	6703680	UI-H-BW0-ajf-e-04-0-Uls1 cDNA, 3' end /clone=IMAGE:2731495 /clone_end=3'	-1	TCTGTCTGAAACTCTTTCTCTCTGA GAATTAAATTCCAATGGACCGT
5841	db mining	Hs.255600	AW297026	6703682	UI-H-BW0-ajf-e-06-0-Uls1 cDNA, 3' end /clone=IMAGE:2731499 /clone_end=3'	-1	GATCTGTGTTTCTCCAAAAGAAG ATCATCTTCCAGAAAAGAGGAT
5842	db mining	Hs.255601	AW297030	6703686	UI-H-BW0-ajf-e-10-0-Uls1 cDNA, 3' end /clone=IMAGE:2731507 /clone_end=3'	-1	TTCCATATGTCACTGTATCTGCCTGG CATTACCCCTCTAAACACACACA
5843	db mining	Hs.288403	AW297036	6703682	AV757131 cDNA, 5' end /clone=BMFAKG04 /clone_end=5'	-1	GCTCACTACCACCTCTCAAATCCAG CTAAAAGCATCACGGCCTCAATGA
5844	db mining	Hs.255614	AW297162	6703808	HNC68-1-F10.R cDNA	-1	GTCCTGGTTGTTAGCTTCCGATCCT CCACACATTGAAACCTAAGCATA
5845	db mining	Hs.255615	AW297175	6703811	UI-H-BW0-ajd-c-04-0-Uls1 cDNA, 3' end /clone=IMAGE:2731375 /clone_end=3'	-1	GGGCAATGGAGGACACAGACTCTCA ACTTCAAGAGGTGTTCATAGGTG
5846	db mining	Hs.255618	AW297199	6703835	UI-H-BW0-ajd-e-07-0-Uls1 cDNA, 3' end /clone=IMAGE:2731477 /clone_end=3'	-1	AGCTGAGGTACGACAAACACAT ATATGCAGATTATCAGCAATAAA
5847	db mining	Hs.255617	AW297201	6703837	7k38c02.x1 cDNA, 3' end /clone=IMAGE:3477507 /clone_end=3'	-1	CCTGCCAGGGTTTCGGAAGTCGC AGGTCGAAAATCCTCCGCATAC
5848	db mining	Hs.255621	AW297220	6703856	UI-H-BW0-ajd-g-09-0-Uls1 cDNA, 3' end /clone=IMAGE:2731577 /clone_end=3'	-1	CTTCTCTGAAATGGTACGCCCTAACT TGCATTTCTGAGAAGCCAAACAAA
5849	db mining	Hs.255622	AW297233	6703869	UI-H-BW0-aji-a-03-0-Uls1 cDNA, 3' end /clone=IMAGE:2731684 /clone_end=3'	-1	AGTTTCTGGCTAAGTCACCTCTTAA GGAGATCCCTGTAAAATTCCACCT
5850	db mining	NA	AW297255	6703891	UI-H-BW0-aji-c-04-0-Uls1 NCL_CGAP_Sub6 cDNA clone IMAGE:2731782 3', mRNA sequence	-1	CAGATTAACCCCCATCCCGCCCT CACCGAGGTGTACAACCTGTGCC
5851	db mining	Hs.48820	AW297262	6703898	TAFII105 mRNA, partial /cds=(0,2405)	-1	AGCAAATTACTCTGCCTGGAAATAAA ATTCTGTCACTTCAGCATCTCT
5852	db mining	Hs.255626	AW297265	6703901	UI-H-BW0-aji-d-02-0-Uls1 cDNA, 3' end /clone=IMAGE:2731826 /clone_end=3'	-1	TCAGGCACTGTATAGGTGGCGAGG ACACAAATGATAGGCAAAGTAGTACA

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5853	db mining	Hs.255630	AW297294	6703930	UI-H-BW0-ajj-f-09-0-Uls1 cDNA, 3' end /clone=IMAGE:2731936 /clone_end=3'	-1	ACAGACCCAAACCTCACAGAGTGAAA GGGGACTTCTCACAGAGTGAAA
5854	db mining	Hs.255632	AW297313	6703949	7k46n07.x1 cDNA, 3' end /clone=IMAGE:3478525 /clone_end=3'	-1	TTGCTTCAGACTTTAACACAATCCT AGAAGCCAGAAAACAATGAAGAAA
5855	db mining	Hs.255633	AW297317	6703953	UI-H-BW0-ajj-h-12-0-Uls1 cDNA, 3' end /clone=IMAGE:2732038 /clone_end=3'	-1	TTCTGTCAAGGCTTCAAAGAGACTT CCATAGTTTGGAACTGGAGTC
5856	db mining	Hs.255634	AW297318	6703954	UI-H-BW0-air-a-01-0-Uls1 cDNA, 3' end /clone=IMAGE:2730121 /clone_end=3'	-1	GATATATTGAAGGTCAAGAGGAGAGC TAAACAGGTATGCCACTGGGTCT
5857	db mining	Hs.255635	AW297328	6703964	UI-H-BW0-air-a-11-0-Uls1 cDNA, 3' end /clone=IMAGE:2730141 /clone_end=3'	-1	AGGCTTGTGAGTATTCCCTTGATT CCTGCTTCTGTCTTTAAATCA
5858	Table 3A	Hs.255637	AW297339	6703975	UI-H-BW0-air-c-03-0-Uls1 cDNA, 3' end /clone=IMAGE:2730221 /clone_end=3'	-1	ACACACAAAAGAAAATAGAAGAGTCT TTTCTGCCTGGGGATCTGCA
5859	db mining	NA	AW297356	6703992	UI-H-BW0-air-d-08-0-Uls1 NCI_CGAP_Sub6 cDNA clone IMAGE:2730278 3', mRNA sequence	-1	ACACCCAGCACCCACAGGGAAAGAAA TAATTCCACAGAGCTAAGTATCCCA
5860	db mining	Hs.330185	AW297367	6704003	UI-H-BW0-air-f-01-0-Uls1 cDNA, 3' end /clone=IMAGE:2730361 /clone_end=3'	-1	TGTGCCTGTGCTCCAGCCTCTCC TATGTGTGTAACCTCAATAAAACC
5861	db mining	Hs.255644	AW297374	6704010	UI-H-BW0-air-f-08-0-Uls1 cDNA, 3' end /clone=IMAGE:2730375 /clone_end=3'	-1	ACCGAGTGTACCGCAAGAGGTGTA AAATCCAGGTTCATGTTGCACAC
5862	db mining	Hs.255645	AW297384	6704020	UI-H-BW0-air-g-08-0-Uls1 cDNA, 3' end /clone=IMAGE:2730423 /clone_end=3'	-1	TCCTGATTCTCAAAGTACCCCCCTTCC CTACAACCTAACATGCTTTGTCT
5863	db mining	Hs.255646	AW297390	6704026	UI-H-BW0-air-h-05-0-Uls1 cDNA, 3' end /clone=IMAGE:2730465 /clone_end=3'	-1	CCATGATTTCCAATGGACAAGCAC TATTAACATGGGACTGTATTCTCT
5864	Table 3A	Hs.255647	AW297400	6704036	UI-H-BW0-als-a-05-0-Uls1 cDNA, 3' end /clone=IMAGE:2730152 /clone_end=3'	-1	AATAGAACTGTAGCCCAGTGATT GGCTGGCAGGGTTAAGGAAGTGGG
5865	db mining	Hs.255648	AW297401	6704037	UI-H-BW0-als-a-08-0-Uls1 cDNA, 3' end /clone=IMAGE:2730154 /clone_end=3'	-1	TCCCAGGAGAGTCACATTCTTTTC ACTAAATAAGGAGGGAAAGAAAAAA
5866	db mining	Hs.255649	AW297407	6704043	UI-H-BW0-als-b-02-0-Uls1 cDNA, 3' end /clone=IMAGE:2730194 /clone_end=3'	-1	GGGTTACCTCACCTCTAGGTTCCCA AGATTCCTAACGTTAAGGAAGCTTT
5867	db mining	Hs.255650	AW297411	6704047	UI-H-BW0-als-b-07-0-Uls1 cDNA, 3' end /clone=IMAGE:2730204 /clone_end=3'	-1	AAAGCGTCCAGTCCCCCTAACCTCAA CACAGAAACATAACAATTTACAA
5868	db mining	Hs.255653	AW297426	6704062	UI-H-BW0-als-c-12-0-Uls1 cDNA, 3' end /clone=IMAGE:2730262 /clone_end=3'	-1	CCCAAGGGCTCTCACCTGAAAGAAT TGTAGGGTTTCAGATCAGCTAAA
5869	db mining	Hs.255657	AW297443	6704079	UI-H-BW0-als-e-09-0-Uls1 cDNA, 3' end /clone=IMAGE:2730352 /clone_end=3'	-1	TGGCCTCCACCCATTAAACTGTCTTT GCCTAACGACAATAATTCCCAGGA
5870	Table 3A	Hs.255661	AW297522	6704158	UI-H-BW0-aja-e-02-0-Uls1 cDNA, 3' end /clone=IMAGE:2731108 /clone_end=3'	-1	TGACTCTGTGATGCCGTGAAATCGTT AAGTGAAGACTTATCACATTACCG
5871	db mining	Hs.255665	AW297581	6704217	UI-H-BW0-ajg-b-08-0-Uls1 cDNA, 3' end /clone=IMAGE:2731718 /clone_end=3'	-1	ATCCTTCAGATTGAGCTGGGTGTCAG CATTCAATTCCACAAAGGCTACCTG
5872	db mining	Hs.255666	AW297590	6704226	RST6539 cDNA	-1	TGGATAAGCAATATGTTGACTAGTA TGAATGCGATTCCACAGCAGTGA
5873	db mining	Hs.255672	AW297626	6704262	UI-H-BW0-ajj-f-12-0-Uls1 cDNA, 3' end /clone=IMAGE:2731918 /clone_end=3'	-1	TCACTAGCAGAATATAGTGGGATG CCAGTATCCTAGTAGAGCTGACCC
5874	db mining	Hs.255673	AW297636	6704272	UI-H-BW0-ajj-h-03-0-Uls1 cDNA, 3' end /clone=IMAGE:2731996 /clone_end=3'	-1	AGTTCTTCTTACAATGGGGTCTG AAATCCAGGGTTCCACACCAGGG
5875	db mining	Hs.255674	AW297649	6704285	UI-H-BW0-ajh-a-05-0-Uls1 cDNA, 3' end /clone=IMAGE:2731665 /clone_end=3'	-1	CCAAATACTTAGTGTAGTTGACTTGT CTTGGGTTGCACTGTAAAGGAGAG
5876	db mining	Hs.255675	AW297651	6704287	UI-H-BW0-ajh-a-07-0-Uls1 cDNA, 3' end /clone=IMAGE:2731669 /clone_end=3'	-1	CAAGAGTTCCATGCGTCCAGTGTG ACCGGAATTAAATCATGTATGGTGT
5877	db mining	Hs.255677	AW297664	6704300	UI-H-BW0-ajh-b-11-0-Uls1 cDNA, 3' end /clone=IMAGE:2731725 /clone_end=3'	-1	GTTCTAACCCATAAGTGCCTCATAC ATACATTGCTAGTCTAAAGAGCTTT
5878	db mining	Hs.255679	AW297692	6704328	UI-H-BW0-ajh-e-05-0-Uls1 cDNA, 3' end /clone=IMAGE:2731857 /clone_end=3'	-1	ACCGGCTAATTGTGACTGGCTGT TTGAAAATAATCCTCTGTGT
5879	db mining	Hs.255681	AW297694	6704330	UI-H-BW0-ajh-e-07-0-Uls1 cDNA, 3' end /clone=IMAGE:2731861 /clone_end=3'	-1	TGGTGGGACTATGTGTTATTCTGTGTA TACTTGCAGTGGGTAGATGTCACT

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5880	db mining	Hs.255682	AW297698	6704334	UI-H-BW0-ajh-e-11-0-U1.s1 cDNA, 3' end /clone=IMAGE:2731869 /clone_end=3'	-1	ACTTCCCTACCTCACAGGTTAGGATT CAAAGTGTGTATCCCCCATTGTG
5881	db mining	Hs.255686	AW297728	6704364	UI-H-BW0-aly-a-01-0-U1.s1 cDNA, 3' end /clone=IMAGE:2730888 /clone_end=3'	-1	GGGTGCTTACAGGATTCTTGGAAAT GTGTAGTGGATGCTGGCTCTAGGG
5882	db mining	Hs.255688	AW297749	6704385	UI-H-BW0-aly-c-03-0-U1.s1 cDNA, 3' end /clone=IMAGE:2730988 /clone_end=3'	-1	ACAGAAGCAGGGGGTCAGAAAGTTT CATAAAGGAGGTCTTGGAACAAA
5883	db mining	Hs.342530	AW297756	6704392	UI-H-BW0-aly-d-01-0-U1.s1 cDNA, 3' end /clone=IMAGE:2731032 /clone_end=3'	-1	CTATTGTGTGGGTTGCCTTGCTTAC TCAACTCAAATATTACCAACCCC
5884	db mining	Hs.255691	AW297760	6704416	UI-H-BW0-aly-e-11-0-U1.s1 cDNA, 3' end /clone=IMAGE:2731100 /clone_end=3'	-1	CAGGTGTGCTTACTGGCAGGAACCG AGGGAATAAATAAGATCACTGGAA
5885	db mining	Hs.255692	AW297781	6704417	UI-H-BW0-aly-e-12-0-U1.s1 cDNA, 3' end /clone=IMAGE:2731102 /clone_end=3'	-1	ACCAGCCTTATGTGTGGGTATTCA ATACTCTGACACATTATACTGTA
5886	db mining	Hs.255693	AW297785	6704421	UI-H-BW0-aly-f-04-0-U1.s1 cDNA, 3' end /clone=IMAGE:2731134 /clone_end=3'	-1	GGGCATTGTTACCCCCCTCCACCA CCATCCCCATTAAAGGCTTCGGGG
5887	Table 3A	Hs.255695	AW297813	6704438	UI-H-BW0-aly-g-09-0-U1.s1 cDNA, 3' end /clone=IMAGE:2731192 /clone_end=3'	-1	CTGTATCTACAACCTCTGACTTCAGA TTTTGTCTCTCAAAACAGCCT
5888	Table 3A	Hs.255697	AW297827	6704452	UI-H-BW0-aly-h-11-0-U1.s1 cDNA, 3' end /clone=IMAGE:2731244 /clone_end=3'	-1	AGCAAGACTAAACCACTAATTACTATT ATCTGACCCAGGAAAATCCGCC
5889	db mining	Hs.255698	AW297843	6704468	UI-H-BW1-aoa-c-05-0-U1.s1 cDNA, 3' end /clone=IMAGE:3083913 /clone_end=3'	-1	TGGATAGTTGCTCAATGTAGCAGTGA TGTCTTGGAAATTGCCAGCAGAGC
5890	db mining	Hs.328317	AW297929	6704585	yg18e06.s1 cDNA, 3' end /clone=IMAGE:32551 /clone_end=3'	-1	CCAACAGATTCTGCTTACCCCTGAGG TGAAGCCTCGTTGAGAACAAAT
5891	db mining	Hs.255705	AW297949	6704585	UI-H-BW0-ajh-d-11-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732229 /clone_end=3'	-1	CAACCTCTGTTGAATTGATTTACTA CTCATCAGGGTCAATGCACAAGCA
5892	db mining	Hs.255706	AW297951	6704587	UI-H-BW0-ajn-e-01-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732257 /clone_end=3'	-1	ACATTCAAACGCCAGAATATGACTG TAAAACAGCGAAGTGTCTCTTTC
5893	db mining	Hs.255708	AW297970	6704606	UI-H-BW0-ajh-f-10-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732323 /clone_end=3'	-1	TCTTCCGGAAATGTGATGTGTTTTT CACTGGTTCTAATTCTGTCTTCC
5894	db mining	Hs.255710	AW297974	6704610	UI-H-BW0-ajn-g-02-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732355 /clone_end=3'	-1	ACTTATTAAATTCTCACCTCAGCCTCA GGGATGTATGAGGGAAAGGACAT
5895	db mining	Hs.255713	AW297994	6704630	UI-H-BW0-ajh-h-11-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732421 /clone_end=3'	-1	ACATTCTGTCAATTAGTGAATAAGAA GCTGAGGTGTGACTAAGAACACAA
5896	db mining	Hs.255717	AW298042	6704678	UI-H-BW0-ajp-e-07-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732629 /clone_end=3'	-1	CCTCTTGTAAAAATCAAGAACAGGT TAGATTAAAGCAGTAAATCCTAGACT
5897	db mining	Hs.330189	AW298048	6704684	UI-H-BW0-ajp-f-01-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732665 /clone_end=3'	-1	TCCTGGCCTTTGTGGGTTTTAATTC CCTTACCTTTCCCTTTGGAT
5898	db mining	Hs.255721	AW298073	6704709	UI-H-BW0-ajp-h-05-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732769 /clone_end=3'	-1	ACTGCTGCAACTACAATTCTCAGATA GTCCCATTTGTTAAATCACGCAT
5899	db mining	Hs.342533	AW298095	6704731	UI-H-BW0-ajs-b-12-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732878 /clone_end=3'	-1	CCTCCCTCTGGCTGTAGGTTCTGT GGCTATAAAACAAATCATAACTTTT
5900	db mining	Hs.255725	AW298108	6704742	UI-H-BW0-ajs-c-07-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732916 /clone_end=3'	-1	TTAAATGCTCCCTGGCTCTCCCTGG GTTTCAGTTCTATCCATGCCCTG
5901	db mining	Hs.255726	AW298110	6704746	UI-H-BW0-ajs-c-11-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732924 /clone_end=3'	-1	TTGTTCTCCTCCCAAGCTCTGGTC TATTTGGCTTTTCAGCTCTGTGC
5902	db mining	Hs.255727	AW298123	6704759	UI-H-BW0-ajs-e-01-0-U1.s1 cDNA, 3' end /clone=IMAGE:2733000 /clone_end=3'	-1	GCATTCAGGGACACAAATGGCCAT GGCAGAGACCACTAATGCCAGATA
5903	db mining	Hs.255736	AW298201	6704837	UI-H-BW0-ajt-d-08-0-U1.s1 cDNA, 3' end /clone=IMAGE:2732987 /clone_end=3'	-1	TTTATCCCGCTTTAACCTTGTGTTGC TTGGTACTTTCTGTGGTTACA
5904	db mining	NA	AW298208	6704844	UI-H-BW0-ajt-e-05-0-U1.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2733009 3, mRNA sequence	-1	CACGCACCCAACCCCCACTGCTCCT CTCCATCCAGATGTTCGTCAGAG
5905	db mining	Hs.255740	AW298234	6704870	UI-H-BW0-ajt-g-09-0-U1.s1 cDNA, 3' end /clone=IMAGE:2733113 /clone_end=3'	-1	TTTGGGGCAATTAAATGGTTAAGTG TAGGAAAATCCACTTACAGTGT
5906	db mining	Hs.330191	AW298238	6704874	UI-H-BW0-ajt-h-04-0-U1.s1 cDNA, 3' end /clone=IMAGE:2733151 /clone_end=3'	-1	GGCTTTGATTTCCATTGGGGTCC CCCGCTTCCCATTTGGTTTTT

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5907	db mining	Hs.255743	AW298239	6704875	UI-H-BW0-ajl-h-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2733153 /clone_end=3'	-1	GACAGTTGGGGAGGGATTGAAGG TCTCGTCAAGAGAACAGAAAACC
5908	db mining	NA	AW298271	6704994	UI-H-BW0-ajk-d-01-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732184 /clone_end=3'	-1	AGGGGCCTTTACCGGTTGTTTCC CTTAAATTTAAAGGAATTGAATT
5909	db mining	Hs.183669	AW298312	6705035	mRNA for KIAA1271 protein, partial cds /cds=(72,1700)	-1	TCCCTTTCTGTCACTGTGAAGCGA TGAATAAACCTGGGTAGATCCA
5910	db mining	Hs.302681	AW298348	6704908	7j80e10.x1 cDNA, 3' end /clone=IMAGE:3392778 /clone_end=3'	-1	CCTAGAAATTATATAACAGGGATAAAT GAGGCACTGAAGGTGGGAGAAC
5911	db mining	Hs.255746	AW298349	6704909	UI-H-BW0-ajl-c-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731795 /clone_end=3'	-1	ACGACAAACTGCACAGTAAATATCAC AAACACGGAAATACCACAGTGTCT
5912	db mining	Hs.255747	AW298355	6704915	UI-H-BW0-ajl-d-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731835 /clone_end=3'	-1	ACCATGACTTGGCAAAGAGTTCAAG AGAGGGCATAATCAAAGTAACCA
5913	db mining	Hs.255749	AW298388	6704948	UI-H-BW0-ajl-g-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731983 /clone_end=3'	-1	GATAATCAAGGGAAAGAGCTTCAGC AGAGCTCCTAGGTTTTCAAAAAA
5914	Table 3A	Hs.313413	AW298430	6705066	602721745F1 cDNA, 5' end /clone=IMAGE:4838506 /clone_end=5'	-1	GCTCAGGGGACAGCTATTCTTTCA AAGCGTTTACCGACTGGATCACCT
5915	db mining	Hs.255762	AW298437	6705073	UI-H-BW0-ajl-d-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732199 /clone_end=3'	-1	TGAGAGCTTCCCTCCTACGATC CAACCATGTCAAACATTCTACCA
5916	db mining	Hs.255763	AW298445	6705081	UI-H-BW0-ajl-e-07-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732245 /clone_end=3'	-1	TGTGCCAACGATGATTCTTGAGT AAATTCCTAACGTCACAGAAAGTT
5917	db mining	Hs.255764	AW298447	6705083	UI-H-BW0-ajl-e-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732249 /clone_end=3'	-1	AGTCAACATGGAGCAAGTGAGCTAAG GAAGTAATGAAACTGTTGGAGA
5918	db mining	Hs.255766	AW298482	6705118	UI-H-BW0-ajl-h-11-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732397 /clone_end=3'	-1	AGCTCAGGTCTCCCTCATCTGTTAG TTTCTGGAGTCTGTTCTCATACT
5919	db mining	Hs.255767	AW298489	6705125	UI-H-BW0-ajm-a-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732078 /clone_end=3'	-1	AAACATACTCCTCTCACCAGCACTC AGACATTGTATCCAGAGAAAGCT
5920	db mining	Hs.255768	AW298490	6705126	UI-H-BW0-ajm-a-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732080 /clone_end=3'	-1	AGCTGTCAATTGTTAACGCTGTGA TCTTCTTTCCAGTTAACAGTT
5921	db mining	Hs.255769	AW298494	6705130	UI-H-BW0-ajm-b-01-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732112 /clone_end=3'	-1	TGTCTCTCAACCCACTTGTGGTTT TACACTGTAAATTACACTATTGTC
5922	db mining	Hs.132781	AW298502	6705138	class I cytokine receptor (WSX-1), mRNA /cds=(138,2048)	-1	GTGTGTATGGTTGGGCTAG GACAGGTTGGGGATGCCCGTAG
5923	db mining	Hs.255770	AW298503	6705139	UI-H-BW0-ajm-b-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732134 /clone_end=3'	-1	CTGTGTTGACTATTGAAAACCTTAA ATTGGGATGCCAAAGTTACTCT
5924	db mining	Hs.255772	AW298510	6705146	UI-H-BW0-ajm-c-11-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732180 /clone_end=3'	-1	GGTTGTATCAAAGAACCTCCACATCC ATATTGAATAAACTCCCAGTAGCC
5925	db mining	Hs.255777	AW298559	6705195	UI-H-BW0-ajm-h-04-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732408 /clone_end=3'	-1	GGCTGCCAGATCTCGTGGGAAAGAA GACCACAGGAGGACTCGGCTCAATG
5926	db mining	Hs.255779	AW298607	6705243	UI-H-BW0-ajr-d-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732615 /clone_end=3'	-1	TGAAAAAAATGATAGCAGCCAACCTGA CAGAAGAACCCAGCATCACATTC
5927	db mining	Hs.255782	AW298616	6705252	UI-H-BW0-ajr-e-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732659 /clone_end=3'	-1	TTGGTTTGGGGATTGGGAAGTCTTA AGCCAAATTGTCCTCCGGTCTCCCC
5928	db mining	Hs.255783	AW298627	6705263	UI-H-BW0-ajr-f-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732707 /clone_end=3'	-1	GCCCTATATCTAGTGAAGCAGGTGTG GCAATCAGGAAGGGATTGATATT
5929	db mining	Hs.255784	AW298632	6705268	UI-H-BW0-ajr-g-04-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732743 /clone_end=3'	-1	TGCACGCAATGCTTGAAGTGTCCCAGGTATTAGTTCAAGTAAATT
5930	db mining	Hs.255785	AW298647	6705283	UI-H-BW0-ajr-h-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732801 /clone_end=3'	-1	CTGTAGGTATGAGCTGCCAGGATCCA GGTGTGACTCGGTATTCTAGGG
5931	db mining	Hs.255788	AW298675	6705311	UI-H-BW0-ajo-c-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732524 /clone_end=3'	-1	TCCCATTTGGGGGTGGGCTGTTAA ATTTGACTCCCTGTTAAACCC
5932	db mining	Hs.255794	AW298720	6705356	UI-H-BW0-ajo-g-07-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732724 /clone_end=3'	-1	CCACTTGCATCTCTGGGGTTCT TTCCCTTCTTCTGTTCAAGGC
5933	db mining	Hs.255797	AW298752	6705388	UI-H-BW0-ajq-b-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732506 /clone_end=3'	-1	TGGGTAATCAACACTCAACCATCAAC AAACACTCTCATTCAGGCACTG
5934	db mining	Hs.255799	AW298806	6705442	RC4-MT0235-061200-011-e11 cDNA	-1	AGGAGAAATAATTAGAGTGGCACACT AGCATGATGGTAAACATTCTGTCA

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5935	Table 3A	Hs.157396	AW300500	6710177	xs66c06.x1 cDNA, 3' end /clone=IMAGE:2774602 /clone_end=3'	-1	AGGAGTTCAAGAACAGCAGAGATTCCA GGTCCATGCACCAAAGCTCATGTG
5936	Table 3A	Hs.262789	AW300868	6710545	xk07d09.x1 cDNA, 3' end /clone=IMAGE:2666033 /clone_end=3'	-1	CTTGTCCCTCTCCTGATCCAGGGCTCC AGTGCCCAGTCCAGTGCCTTGGT
5937	db mining	Hs.255880	AW337887	6834513	he12d07.x1 cDNA, 3' end /clone=IMAGE:2918787 /clone_end=3'	-1	GCATCTCCCCGCTGTCAGCCTCAGC CCTCTCCTACCAAAATCTCTTCGA
5938	Table 3A	Hs.328348	AW338115	6834741	tp39g05.x1 cDNA, 3' end /clone=IMAGE:2190200 /clone_end=3'	-1	GCGCTTCCCATTGACCAGTTGACC CTGGTTGAATAAGAGAAAGTGC
5939	db mining	Hs.255920	AW339530	6836156	he13d09.x1 cDNA, 3' end /clone=IMAGE:2918897 /clone_end=3'	-1	AGCCCATTAAGAACCTTGGCAAAATG TCAGACCTTAAGACTTCCACTAT
5940	Table 3A	Hs.255927	AW339651	6836277	he15g04.x1 cDNA, 3' end /clone=IMAGE:2919126 /clone_end=3'	-1	TCAAGACAAAGGAAGCTGAAAATA AGAGCTGAGAAAGGAAGAACTTT
5941	Table 3A	Hs.207995	AW340421	6837047	hc96h02.x1 cDNA, 3' end /clone=IMAGE:2907891 /clone_end=3'	-1	ATATACATACAAATCTAAGCTCAAG AAGCTTAAGAAACCCCTTAGGGG
5942	Table 3A	Hs.256031	AW341086	6837631	xz92h04.x1 cDNA, 3' end /clone=IMAGE:2871703 /clone_end=3'	-1	GGGCAATTACATCGGGACTCGTTTC ATCTCTAGACCTTCACCTACCTGA
5943	Table 3A	Hs.283667	AW341449	6838075	arginyl aminopeptidase (aminopeptidase B) (RNPEP), mRNA /cds=(9,1982)	-1	AGCTCTGGAGTGCCCTCCCTCCAAA TAAAGTATTTAACGAAACACTGA
5944	Table 3A	Hs.337986	AW440517	6975823	Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336,1494)	-1	GCCAGTCTCTATGTGTCTTAATCCCT TGTCTTCATTAAAAGCAAAACTA
5945	db mining	Hs.256956	AW440813	6976044	he03b05.x1 cDNA, 3' end /clone=IMAGE:2917905 /clone_end=3'	-1	CCCTCAGGCATAGAAATTGAATCTGA AATGGCTGATGATAAAGCAAAGGC
5946	db mining	Hs.313573	AW440817	6976048	he03c02.x1 cDNA, 3' end /clone=IMAGE:2917922 /clone_end=3'	-1	CAGCCCTGCCTGAGTTTGACACCT GCATCCCTCCCTGCCTCACCTCAC
5947	Table 3A	Hs.256961	AW440866	6976172	he05f02.x1 cDNA, 3' end /clone=IMAGE:2918139 /clone_end=3'	-1	AGAGCAGGAGAAATCCTACTGCATTA TTAATCTGAAAGCACAAGGACAGC
5948	Table 3A	Hs.173730	AW440869	6976175	Mediterranean fever (MEFV), mRNA /cds=(41,2386)	-1	CTGCTTGGTTGTATGGGAAATCT GCGGGTTGTGGAATATTAGGTCT
5949	Table 3A	Hs.118446	AW440965	6976271	HNC35-1-D12.R cDNA	-1	TGGGATTATAGGGGGAGACAGGAGT TGTGAAATTACAGGAGAGGTTCACT
5950	db mining	Hs.118446	AW440965	6976271	HNC35-1-D12.R cDNA	-1	TGGGATTATAGGGGGAGACAGGAGT TGTGAAATTACAGGAGAGGTTCACT
5951	Table 3A	Hs.256971	AW440974	6976280	he08e12.x1 cDNA, 3' end /clone=IMAGE:2918254 /clone_end=3'	-1	CTGAGAAAAGGAGTGTCTCTCTCTG CTCCCAAATTCAGTAGCTTCCA
5952	Table 3A	Hs.342632	AW444482	6986244	UI-H-BI3-akb-e-05-0-U1.s1 cDNA, 3' end /clone=IMAGE:2733777 /clone_end=3'	-1	TCGAGGTTCTCCCAAGAAAAGCCCA ATCTTATAAACTGTTACTTCCCT
5953	Table 3A	Hs.250	AW444632	6986394	xanthene dehydrogenase (XDH), mRNA /cds=(81,4082)	-1	TGCAATGAGGCAGTGGGTAAGGTT AAATCCTCTAACCGTCTTGAATCA
5954	Table 3A	Hs.335815	AW444812	6986574	UI-H-BI3-ajy-d-11-0-U1.s1 cDNA, 3' end /clone=IMAGE:2733380 /clone_end=3'	-1	TGCGAACCTCAACTCCCTGATGGCGA TAATCTCTGGATGAAATATGAGCC
5955	Table 3A	Hs.99665	AW444899	6986691	UI-H-BI3-ajz-d-07-0-U1.s1 cDNA, 3' end /clone=IMAGE:2733373 /clone_end=3'	-1	TTGTGCTCTGATACGACGTTGCCAC AGTTAACCGCTCTGATCTCTCT
5956	Table 3A	Hs.257283	AW450350	6991126	UI-H-BI3-akn-c-01-0-U1.s1 cDNA, 3' end /clone=IMAGE:2734825 /clone_end=3'	-1	CAAGCCTAACCTTCCAAACACTCCGC GACGCAACCCCTTCCCTTCC
5957	Table 3A	Hs.313715	AW450835	6991611	UI-H-BI3-alf-f-06-0-U1.s1 cDNA, 3' end /clone=IMAGE:2736539 /clone_end=3'	-1	CACGGTTAGAGTCACCAAACCTGTAT TTCAGGGGACATCTTCCAGCTCC
5958	Table 3A	Hs.199014	AW450874	6991650	601499703F1 cDNA, 5' end /clone=IMAGE:3901440 /clone_end=5'	-1	CCAAAGGCTCACTACCCCTGTGCGTT GTCCAGCACAGACACTATGTGC
5959	Table 3A	Hs.342873	AW451293	6992069	RC3-HT0230-130100-014-g06 cDNA	-1	TGCTTGGGAAATTGGTTGTAAACC TAAATAGCCCTTATTCTGGGGA
5960	Table 3A	Hs.101370	AW452023	6992799	AL583391 cDNA /clone=CSODL012YA12-(3-prime)	-1	CATCTGCTGAGCAGTGTGCTGTGCA ACCTCTCTAGGTCTCTCTATG
5961	Table 3A	Hs.342735	AW452096	6992953	UI-H-BI3-alb-d-02-0-U1.s1 cDNA, 3' end /clone=IMAGE:3068186 /clone_end=3'	-1	CTTCTGCTGAAGCTGCCCCCATGA CTCCCTCTTGTGCAAAGCATG
5962	Table 3A	NA	AW452467	6993243	UI-H-BI3-als-e-09-0-U1.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:3058632 3', mRNA sequence	-1	GAAATGAGTTGGTGTCTCACAGAAAT GAGGATCCCCAGAGCCATCTTGC
5963	Table 3A	Hs.257579	AW452513	6993289	UI-H-BW1-ame-b-03-0-U1.s1 cDNA, 3' end /clone=IMAGE:3069628 /clone_end=3'	-1	GTCCTCCCTCCCACTCTGCCTTACC TGGTATCTATGACTGACTGAAAT

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5964	db mining	Hs.257581	AW452528	6993304	UI-H-BW1-ame-c-07-0-U1.s1 cDNA, 3' end /clone=IMAGE:3059684 /clone_end=3'	-1	TGCGAGAGGAAGCAGAGACCACTT GAAACTCGGGTGCATTAAGTCCTTG
5965	db mining	Hs.257582	AW452545	6993321	UI-H-BW1-ame-d-12-0-U1.s1 cDNA, 3' end /clone=IMAGE:3059742 /clone_end=3'	-1	TTAGCCACTGCTATTCTAGGTTCCCTT GATGGAGCCCCACTCCACGCCCTA
5966	db mining	Hs.257630	AW452932	6993708	UI-H-BW1-amd-c-07-0-U1.s1 cDNA, 3' end /clone=IMAGE:3059325 /clone_end=3'	-1	ACCACCCCAGAGGTTGCTGGCTTCCTT AATAAGCTAACCTCCCTTCACC
5967	db mining	Hs.257632	AW452953	6993729	UI-H-BW1-amd-e-04-0-U1.s1 cDNA, 3' end /clone=IMAGE:3059415 /clone_end=3'	-1	AGGGGAGGCCAGTGGTTGGTCAT GGGAAAGTGTCTCATAAAATTCTATT
5968	db mining	Hs.257633	AW452960	6993736	UI-H-BW1-amd-e-11-0-U1.s1 cDNA, 3' end /clone=IMAGE:3059429 /clone_end=3'	-1	GCACCAGACTCTGAACAGGCTGGG AGAGTGAGGCATAACACATGAAAT
5969	db mining	Hs.257636	AW452985	6993761	UI-H-BW1-amd-g-12-0-U1.s1 cDNA, 3' end /clone=IMAGE:3059527 /clone_end=3'	-1	ACACAGTACTTTGTTGAGATGTTGGC TTCTGGTTATGGCATGAATTCT
5970	Table 3A	Hs.257640	AW453021	6993787	UI-H-BW1-ama-c-02-0-U1.s1 cDNA, 3' end /clone=IMAGE:3059290 /clone_end=3'	-1	ACTTATCTTGCACCCATGTTCTT GGATGCCTGCCTCCCTCTTCTAT
5971	db mining	Hs.257644	AW453034	6993810	UI-H-BW1-ama-d-03-0-U1.s1 cDNA, 3' end /clone=IMAGE:3059340 /clone_end=3'	-1	AAACAGGAAGCCTCTCATGAATTGA CCAAGGAGCTACATCGTTCTCTA
5972	db mining	Hs.257645	AW453039	6993815	UI-H-BW1-ama-d-08-0-U1.s1 cDNA, 3' end /clone=IMAGE:3059350 /clone_end=3'	-1	TGAGGAAGAGGAGATTATTAAAGCCC CTTCTTTAGGCTAGGAGTTTCC
5973	Table 3A	Hs.257646	AW453044	6993820	UI-H-BW1-ama-e-01-0-U1.s1 cDNA, 3' end /clone=IMAGE:3059384 /clone_end=3'	-1	GGACACTGGCTTTGTGCAGCTCTTC ATCACAGAGTCTGTTGAGCTAACAA
5974	db mining	Hs.257647	AW453055	6993831	UI-H-BW1-ama-e-12-0-U1.s1 cDNA, 3' end /clone=IMAGE:3059408 /clone_end=3'	-1	ACAGTGATTTCAACCAAGGGCTTTT TCAAACACTACCTCTTAGCTCC
5975	Table 3A	Hs.257667	AW467193	7037299	he07a04.x1 cDNA, 3' end /clone=IMAGE:2918286 /clone_end=3'	-1	GGTGGTGGCTACAAGGGTGAATTGCC TTATGATAATTGACCGTGTCTATAAT
5976	db mining	Hs.257668	AW467208	7037314	he07c09.x1 cDNA, 3' end /clone=IMAGE:2918320 /clone_end=3'	-1	AGCTGGGAGGCCATTACTTTTGTC GAGTCTCTGGAGTTCTAGCAAAA
5977	db mining	Hs.255877	AW467312	7037418	he09b01.x1 cDNA, 3' end /clone=IMAGE:2918473 /clone_end=3'	-1	AGTTGCATTAACGTGAGCTAGATGT GTAAGTTGCTAACGGATGGGTTT
5978	db mining	Hs.257677	AW467338	7037444	he09e07.x1 cDNA, 3' end /clone=IMAGE:2918532 /clone_end=3'	-1	CCTCTAAGGCATTATTAACGTGACAA CATAAAATCTGAACCCAGGTCA
5979	db mining	Hs.257679	AW467385	7037491	he10d12.x1 cDNA, 3' end /clone=IMAGE:2918615 /clone_end=3'	-1	TCACCTCCATCAACTTACTAGCACAT AAAGGGTGGGATTTCATGTTGA
5980	Table 3A	Hs.257680	AW467400	7037506	he10f11.x1 cDNA, 3' end /clone=IMAGE:2918637 /clone_end=3'	-1	CTGGCAAAGGCATGGGTACAACTG CTCTGTGATCTACCTCTGAACAC
5981	db mining	NA	AW467421	7037527	he17b02.x1 NCL_CGAP_CML1 cDNA clone IMAGE:2919243 3' similar to contains Alu repetitive element; con	-1	ACACCTGTGGTATATTGTATCATTCA GTCTGGTTCTCACCCCTCTCAA
5982	Table 3A	NA	AW467437	7037543	he17d05.x1 NCL_CGAP_CML1 cDNA clone IMAGE:2919273 3', mRNA sequence	-1	AACCCCTCGTAAGGTTCATCTCCCTT GATTGCAAATGAGTTGTGTGAA
5983	db mining	NA	AW467445	7037551	he17e08.x1 NCL_CGAP_CML1 cDNA clone IMAGE:2919302 3' similar to contains element MSR1 repetitive el	-1	CCCGCTTCACCTCCCTAAATAACTC GTTGCAGGCTAATCCATCAAAT
5984	db mining	NA	AW467448	7037554	he17f02.x1 NCL_CGAP_CML1 cDNA clone IMAGE:2919291 3' similar to contains Alu repetitive element; con	-1	ATTTTGCTCATTACCTGTCAGGAGAA AACCCCTCTCCCCAGTCTCCACT
5985	Table 3A	Hs.257687	AW467501	7037607	he19e06.x1 cDNA, 3' end /clone=IMAGE:2919490 /clone_end=3'	-1	ACCTACTGAATCTCCAGATTGCCAAG TGAAACACAATGGTTGCCCTCTCA
5986	db mining	Hs.257688	AW467571	7037677	he21f02.x1 cDNA, 3' end /clone=IMAGE:2919675 /clone_end=3'	-1	TGCGAAAGCTAATCCCTAGTATGAA TAAACTCAGACCTTGCTCTCC
5987	db mining	Hs.257690	AW467582	7037688	602497524F1 cDNA, 5' end /clone=IMAGE:4611316 /clone_end=5'	-1	AGCCTGAGGTGGGTGAAGAAAATAC CTGCTTATACTGTTCTGGAAACTC
5988	db mining	Hs.266387	AW467607	7037713	he22c05.x1 cDNA, 3' end /clone=IMAGE:2919752 /clone_end=3'	-1	CTTTTCCCTTCATGGTAGTTGCTGC TTAAGTTCTAACATGCCTGCA
5989	Table 3A	Hs.257695	AW467746	7037776	he23d05.x1 cDNA, 3' end /clone=IMAGE:2919849 /clone_end=3'	-1	TGAATGTCAGATGCAAGAACCCATTG ATATGGAGGGCTGAGTGTCTGAAA
5990	Table 3A	Hs.257705	AW467863	7037969	he27c04.x1 cDNA, 3' end /clone=IMAGE:2920230 /clone_end=3'	-1	TGTACTACTTATTATGTTAAACCAT ACACAGGGCTAGAAAGGAAGGGAT

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5991	Table 3A	Hs.257706	AW467864	7037970	he27c05.x1 cDNA, 3' end /clone=IMAGE:2920232/clone_end=3'	-1	TGTAGAAATTGCAGGAGTAGAAAGACCC TTGAAAGATCATTGTCCCTGTGGT
5992	Table 3A	Hs.257709	AW467992	7038098	he30b01.x1 cDNA, 3' end /clone=IMAGE:2920489/clone_end=3'	-1	GCTCAAGTCCCAGCACCTGGGGAA TTCTAACGCTGAGGAAGACAAGGTG
5993	db mining	Hs.257713	AW468139	7038245	he32g11.x1 cDNA, 3' end /clone=IMAGE:2920772/clone_end=3'	-1	TGTTTTATGTCCCTGAGCAAGCAAATT GCTGCAATTAAATCACCAATT
5994	Table 3A	Hs.257716	AW468207	7038313	he34a12.x1 cDNA, 3' end /clone=IMAGE:2920894/clone_end=3'	-1	AGGCCTGATATTGAAAGCTTTGATA CTGAGATCCTATTAACTCAGATGA
5995	db mining	Hs.257719	AW468316	7038422	he36a05.x1 cDNA, 3' end /clone=IMAGE:2921072/clone_end=3'	-1	TGTTAGTTGCTTTGAAATTCTTGG AGGGTACTCTTCAGGGCTTCACA
5996	db mining	Hs.278060	AW468430	7038536	he37h10.x1 cDNA, 3' end /clone=IMAGE:2921251/clone_end=3'	-1	TAGTGATTATCTCCAGGAATCAAGTA CAAACTTTGAAAAAGACTGGAGGT
5997	Table 3A	Hs.257727	AW468431	7038537	he37h11.x1 cDNA, 3' end /clone=IMAGE:2921253/clone_end=3'	-1	TTTGTCCAAGGGCTCAGACTGAAAG AATGCAATGTGAGAGGTATGCCAC
5998	db mining	Hs.330268	AW468459	7038565	he38d05.x1 cDNA, 3' end /clone=IMAGE:2921289/clone_end=3'	-1	TCTGTGAAAATCTTCTGCAAATGTCT TTGCTTGCTTGACTCACGTTT
5999	db mining	Hs.257738	AW468559	7038665	he41a07.x1 cDNA, 3' end /clone=IMAGE:2921556/clone_end=3'	-1	TGTCCTTAACGCACAGATGTTACTTC AGCACCACAAGGACTGTTGATGGA
6000	Table 3A	Hs.257743	AW468621	7038727	he42e03.x1 cDNA, 3' end /clone=IMAGE:2921692/clone_end=3'	-1	CAGTCAGATGTTGAAATTGGGGGTA GAGGGATTATAGAGTTGTGTGCT
6001	Table 3A	Hs.122116	AW469546	7039652	hd19e09.x1 cDNA, 3' end /clone=IMAGE:2909992/clone_end=3'	-1	AAAGGAGGGACTATGGCATCAAACA GCCTCTTCAGCACAGTGACACCATG
6002	Table 3A	Hs.80818	AW510795	7148873	hypothetical protein (FLJ20015), mRNA /cds=(31,522)	-1	ACCCAGTTGTGCATAGTCATGATC CTCTATAAAACCACTTTGTGGA
6003	Table 3A	Hs.193669	AW512498	7150576	hypothetical protein DKFZp586J1119 (DKFZp586J1119), mRNA /cds=(27,2153)	-1	CTGTCGGGCTCTGAAGCGAGCTGGT TTAGTTGAGAGATGCTCTGTTT
6004	Table 3A	Hs.42915	AW572538	7237271	ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA /cds=(74,1258)	-1	TGGAATGGACTCTAAAACAATGAAA GAGCATTTATCGTTGCTCTTGA
6005	Table 3A	Hs.342858	AW572930	7237663	hf17f07.x1 cDNA, 3' end /clone=IMAGE:2932165/clone_end=3'	-1	TCACTACCTCAATTGTTACAAGGT GGATATGGCAGCAACAGATACT
6006	Table 3A	Hs.325991	AW573211	7237944	602679187F1 cDNA, 5' end /clone=IMAGE:4812093/clone_end=5'	-1	CTAGGCCGGATGGGCCAGAGAAGGA GAACCATGGCAGGAGCCGGAAGCAG
6007	db mining	Hs.258933	AW589231	7276337	he27g09.x1 cDNA, 3' end /clone=IMAGE:2920288/clone_end=3'	-1	AAATGTTGAGCACTGTTCAATAACA GCACTAATTGTGTGTTCATGGCT
6008	Table 3A	Hs.304925	AW592876	7280068	hg04d05.x1 cDNA, 3' end /clone=IMAGE:2944617/clone_end=3'	-1	CTGGCACATCCAGGTTTAGAGCAGG CAGCCTGAGATTCAAAAATGAGG
6009	Table 3A	Hs.298654	AW614181	7319367	hg77d03.x1 cDNA, 3' end /clone=IMAGE:2951621/clone_end=3'	-1	GGAGCGGAATACAGTAAAAGCACTG GACTGACCTAAGAGTTGTTCTGC
6010	Table 3A	Hs.259842	AW614193	7319379	cDNA FLJ11025 fis, clone PLACE1003968, moderately similar to 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT /cds=(159,1145)	-1	ACACCATTTCAGCGTGGATCACAGA CAGCTCTCCCTTATATCCCAGCA
6011	Table 3A	Hs.342967	AW629176	7375966	602819939F1 cDNA, 5' end /clone=IMAGE:4745649/clone_end=5'	-1	CCACCTTGCTGCCTTTGAAACACTC AGGAAATATAGTTGGCTAAAATCG
6012	Table 3A	Hs.140720	AW629485	7376275	FRAT2 mRNA, complete cds /cds=(129,830)	-1	CACTTCGCAACGGAGTGTGTTGAAATT GTGGTGGCTCTGATTATAGGATT
6013	db mining	Hs.175437	AW771958	7704007	hn66h10.x1 cDNA, 3' end /clone=IMAGE:3032897/clone_end=3'	-1	GCTTGGCAGATGGATTAAACCTGTCTT CTTTGGAGCCAGATCAATATCTA
6014	Table 3A	Hs.151393	AW778854	7793457	glutamate-cysteine ligase, catalytic subunit (GCLC), mRNA /cds=(92,2005)	-1	AGAATGCCCTGGTTTCGTTGCAATT TGCTTGTAAATCAGGTTGTAAC
6015	Table 3A	Hs.109441	AW780057	7794660	cDNA FLJ14235 fis, clone NT2RP4000167 /cds=(82,2172)	-1	TTCTGAACATTTAGTCAGCTACAC AGGTTGGAAAACCTCTGTGGGG
6016	Table 3A	Hs.343475	AW873028	8007081	601556208T1 cDNA, 3' end /clone=IMAGE:3826392/clone_end=3'	-1	TGCAAGTGGATGGTTGGTATCACTG TAAATAAAAAGAGGGCCTGGGAAA
6017	Table 3A	Hs.166338	AW873324	8007377	hf92a07.x1 cDNA, 3' end /clone=IMAGE:3009396/clone_end=3'	-1	GTGGCTTTCTGTTGACGCCAAAGGT TACTCCCTCTGCCTCACCATAAAA

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6018	Table 3A	Hs.90960	AW873326	8007379	602563938F1 cDNA, 5' end /clone=IMAGE:4688769 /clone_end=5'	-1	ACCTCCTACGTCTGTTTCTGGCTGT GGTGAATTGGATTTAACCTTA
6019	Table 3A	Hs.120243	BE044364	8361417	gamma-parvin (PARVG), mRNA /cds=(0,995)	-1	ATCGTTGGATTATCTTTGAACCCCT TGTGAGATCATTTGAGCCGCCT
6020	db mining	Hs.157489	BE047166	8364219	602462536F1 cDNA, 5' end /clone=IMAGE:4575393 /clone_end=5'	-1	AGCTCCAAAGTGGTTGATGACCAACA GGCTAAAATCATAGTCTAAAT
6021	Table 3A	Hs.82316	BE049439	8366494	interferon-induced, hepatitis C-associated microtubular aggregate protein (44kD) (MTAP44), mRNA /cds=(0,1334)	-1	TCAAGAAAGGAGAAAAACACAGACAAA GAGAAGTATCTAAGACCAAAGGGA
6022	Table 3A	Hs.121587	BE217848	8905166	602637382F1 cDNA, 5' end /clone=IMAGE:4765191 /clone_end=5'	-1	GCATCACGATTGTCTACATAAGTCC AGTCATCTCGCGTTGTTGGC
6023	Table 3A	Hs.5734	BE218938	8906256	meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(395,3145)	-1	ATACAGGGTTCATCCAGAAAGCATT CACTCAGCAAGTTAAAGTCAGT
6024	Table 3A	Hs.203772	BE220869	8908187	FSHD region gene 1 (FRG1), mRNA /cds=(191,967)	-1	AAGTGCCAGATTGATAATCACCAG CCTCTCATCAACTCCTATGTTGC
6025	Table 3A	Hs.73931	BE220959	8908277	major histocompatibility complex, class II, DQ beta 1 (HLA-DQB1), mRNA /cds=(57,842)	-1	ACCCCTGGTCACTGGTGTGTTAAACA TTCTGGCAAGTCACATCAATCAAG
6026	Table 3A	Hs.128675	BE222032	8909271	hr65h11.x1 cDNA, 3' end /clone=IMAGE:3133028 /clone_end=3'	-1	AGCTCTGGAGCCTTGCTTCCCTCAA TACGAGCGGGAACTGCGTTGAGCG
6027	Table 3A	Hs.167988	BE222301	8909619	neural cell adhesion molecule 1 (NCAM1), mRNA /cds=(201,2747)	-1	AAGTTGCTCTGTGCTAAAGCAAGCGT GGGATGATCCTACCTACCTCTAGG
6028	Table 3A	Hs.79914	BE222392	8909710	tumican (LUM), mRNA /cds=(84,1100)	-1	ATTGGGACAGATGCAAGAGAACTGT TAGTGAGTCAGACAAACACATCT
6029	Table 3A	Hs.99237	BE326857	9200633	hr65h08.x1 cDNA, 3' end /clone=IMAGE:3133403 /clone_end=3'	-1	CCCCTACCCCTGAAAGTAATATACT GAAGTCTCATCATACTGTTGGG
6030	Table 3A	Hs.83623	BE328818	9202594	nuclear receptor subfamily 1, group I, member 3 (NR1I3), mRNA /cds=(272,1318)	-1	TGTTTCGTAAATTAAATAGGTCTGGC CCAGAAGACCCACTCAATTGCTT
6031	Table 3A	Hs.27774	BE348809	9260662	602386841F1 cDNA, 5' end /clone=IMAGE:4515730 /clone_end=5'	-1	AGCTAGTGATGTTTGTCCAAGGAA GATTCTGACAACAGCTTCAGCAGA
6032	Table 3A	NA	BE348955	9260808	hs91h01.x1 NCI_CGAP_Kid13 cDNA clone IMAGE:3144625 3', mRNA sequence	-1	ACACAGACATATTGACCGCACACAAAC ACTGAAATGGACTGACTGAGAAA
6033	Table 3A	Hs.56156	BE349148	9261087	601463387F1 cDNA, 5' end /clone=IMAGE:3866512 /clone_end=5'	-1	TGGTTCTGATTGTGTAATGAGCACC TGGATATGTCAATTAAATGCCCA
6034	Table 3A	Hs.315050	BE351010	9262791	ht22g04.x1 cDNA, 3' end /clone=IMAGE:3147510 /clone_end=3'	-1	GGTCATGTACCGTGACTACACCC CTATGATTGGTTGTTGTCAGAAG
6035	Table 3A	Hs.5027	BE379724	9325089	601159415T1 cDNA, 3' end /clone=IMAGE:3511107 /clone_end=3'	-1	TGCTAGTTAGGTCCCTCAGGCATTG ATTGTACAGTTAAACTCCGAGTG
6036	Table 3A	Hs.86437	BE464239	9510014	602411368F1 cDNA, 5' end /clone=IMAGE:4540096 /clone_end=5'	-1	ACAAGCATTTAGATCATAACATGGTA AAGCCTATTACCAGCCAATGTTGT
6037	Table 3A	Hs.127428	BE466500	9512198	Homo sapiens, Similar to homeo box A9, clone MGC:19848 IMAGE:2987818, mRNA, complete cds /cds=(62,880)	-1	GGCCTACTGACCAAATTGTTGTGTTG AGATGATATTAACCTTTGCCAA
6038	Table 3A	Hs.21812	BE487470	9513245	AL562895 cDNA /clone=CSODC021YO20-(3-prime)	-1	AAGTTTGTGCAGCACATTCCCTGAGTG TACGATATTGACCTGTAGGCCAGC
6039	Table 3A	Hs.122575	BE502246	9704654	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4 (EDG4), mRNA /cds=(6,1061)	-1	CGATAGAATTGAAGCAGTCACCGGG GAGGGGTGATAACAGGAGTAAACC
6040	Table 3A	Hs.279522	BE502919	9705327	hz81b08.x1 cDNA, 3' end /clone=IMAGE:3214359 /clone_end=3'	-1	ATAGACTCCAAAGAGGCCTAAC CTGGTTTCTGGCTCAGAAAA
6041	Table 3A	Hs.197766	BE502992	9705400	clone 23932 mRNA sequence /cds=UNKNOWN	-1	CTAAACGAAATTGGGCAGGCCATT GCGTGGTTCTGGATAAGTTC
6042	Table 3A	Hs.61428	BE550944	9792638	602329933F1 cDNA, 5' end /clone=IMAGE:4431248 /clone_end=5'	-1	GCACATGACAGTAAGCGAGGTTTGG GTAATATAGTGAGGATGCCAT
6043	Table 3A	Hs.201792	BE551203	9792895	7b55h12.x1 cDNA, 3' end /clone=IMAGE:3232199 /clone_end=3'	-1	TCCCAGAGTAACTGACAGTATCAAAT AGCAAGAGAGTAGGATGAGGACT
6044	Table 3A	Hs.122655	BE551867	9793559	hypothetical protein MGC14425 (MGC14425), mRNA /cds=(318,688)	-1	ACACAGGAACCGCTTACCCACAGCT CTGCCCGCGTCTCACCGCCATAG
6045	Table 3A	Hs.282091	BE552131	9793823	hw29b05.x1 cDNA, 3' end /clone=IMAGE:3184305 /clone_end=3'	-1	TTCTCCAAGAGAATAACCCATTAAA GGCTAAAATGGAAGCTCCCACT

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6046	Table 3A	Hs.146381	BE613237	9894834	RNA binding motif protein, X chromosome (RBMX), mRNA /cds=(11,1186)	-1	ACTGACCTAGCAGATGTGTGGAAAAG GAATCAGATCTTGAATTCTCTGGG
6047	Table 3A	Hs.4310	BE614297	9895894	eukaryotic translation initiation factor 1A (EIF1A), mRNA /cds=(207,641)	-1	ACAACTCAAGTAAAAGATGTCCTCA GTTTCTGAAGATAACGCACGCTGA
6048	Table 3A	Hs.198802	BE621611	9892551	601493754T1 cDNA, 3' end /clone=IMAGE:3895836 /clone_end=3'	-1	CGCCGACTCGTTGAAAGTTTGTGT GTAGTTGGTTTCGTTGAGTTCT
6049	Table 3A	Hs.324481	BE646433	9970744	EST380617 cDNA	-1	CACCCACCTGGTAGGAAGGTCAATCT TATGCTCAGAACGTCACCCACCA
6050	db mining	Hs.283165	BE646441	9970752	7e86h06.x1 cDNA, 3' end /clone=IMAGE:3292091 /clone_end=3'	-1	CAACTCCTAAAGGGTTGAAGGTTGT GACAATACTGAGGGAACTGATGT
6051	Table 3A	Hs.341573	BE646470	9970781	tc38c11x1 cDNA, 3' end /clone=IMAGE:2066900 /clone_end=3'	-1	AAAACACTCCACCTAAAAGCAGGAA GATGGCAATTCTAAATAGCAGCTA
6052	db mining	Hs.283168	BE646492	9970803	7e87g01.x1 cDNA, 3' end /clone=IMAGE:3292176 /clone_end=3'	-1	GGAGGTTTGATCGTGACTTTTTT GAGATATTGATCTTGTAGTATTGC
6053	Table 3A	Hs.187872	BE646499	9970810	7e87h02.x1 cDNA, 3' end /clone=IMAGE:3292179 /clone_end=3'	-1	TTGTAAGGTTCCGGGGAACTGACTCA ACATGGTTCTCAAACTCGAGGTTG
6054	db mining	Hs.283167	BE646510	9970821	7e88b08.x1 cDNA, 3' end /clone=IMAGE:3292215 /clone_end=3'	-1	TGTGAGTGTATAGGTTACAGTGGAT TCCAAACTGCCACAAAGTGAAGCA
6055	db mining	Hs.283168	BE646569	9970880	7e89c01.x1 cDNA, 3' end /clone=IMAGE:3292320 /clone_end=3'	-1	TCAGCCAGGAGGAAAAGCACTCTGAT TATGAATTGAGCAGAAGGAAACAA
6056	db mining	Hs.283169	BE646617	9970928	7e91b07.x1 cDNA, 3' end /clone=IMAGE:3292501 /clone_end=3'	-1	GTTCCCACTCGTTCTGCCGGAGAAA CCTGCCCTTCAAGCATAATTCAA
6057	db mining	Hs.225200	BE646640	9970951	7e91f08.x1 cDNA, 3' end /clone=IMAGE:3292551 /clone_end=3'	-1	GGGTCCAAGATTATTGATTAATTGG GCACCCGAGAGCTCGAGTCCCCC
6058	Table 3A	Hs.129192	BE670584	10031125	7e36h08.x1 cDNA, 3' end /clone=IMAGE:3284607 /clone_end=3'	-1	GACCACCTGAAAGCAAGTCCTTCA AGTTTCACTGCACATCCAAACCA
6059	Table 3A	Hs.75703	BE670804	10031345	small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386)	-1	TGGTCCACTGTCACTGTTCTTGCT GTTGCAAATACATGGATAACACAT
6060	Table 3A	Hs.195374	BE671815	10032445	7a47c12.x1 cDNA, 3' end /clone=IMAGE:3221878 /clone_end=3'	-1	AGACTCTGAAAAGGAGGGTCGGAG TATTAACACTGGCTGGATGAGAGG
6061	Table 3A	NA	BE672733	10033274	7b75g07.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:3234108 3' similar to TR:O99231 O99231 CYTOCHROME OXIDASE	-1	TGAGAGCACACCATAAATTACAGCA GGAATAAACGAGACACACGAGCA
6062	Table 3A	Hs.77542	BE673364	10033905	602629438F1 cDNA, 5' end /clone=IMAGE:4754432 /clone_end=5'	-1	ACATTCTCTCATTGCTGAAGCTGAT TTGATTGGGTGCTGTTCTCGC
6063	Table 3A	Hs.66357	BE673759	10034300	7d69d02.x1 cDNA, 3' end /clone=IMAGE:3278211 /clone_end=3'	-1	TGAGAAGGTAAGTAGAAAGGGAG ATGATGAGTGAACAATAAGCCTGT
6064	db mining	Hs.283248	BE674662	10035284	7e93g03.x1 cDNA, 3' end /clone=IMAGE:3292756 /clone_end=3'	-1	ACATTATTCCATGGAAATAAGTCATC AGTCAAAGGACTGTAAGGAGTC
6065	Table 3A	Hs.88845	BE674685	10035307	AV733781 cDNA, 5' end /clone=cDAASF08 /clone_end=5'	-1	CGCCGCTCTGGAGACCTGATAACTT AGGCTTGAATAATTGACTTGCT
6066	Table 3A	Hs.171120	BE674709	10035331	7e94f05.x1 cDNA, 3' end /clone=IMAGE:3292833 /clone_end=3'	-1	TGTATGTGCAATATGCTTATGGTAA TTATGGGCAAGAGAAATGGAAACA
6067	db mining	Hs.283249	BE674713	10035335	7e94g02.x1 cDNA, 3' end /clone=IMAGE:3292850 /clone_end=3'	-1	ACCCCTGGAAAGCAGTTGTAAGAA TTAACACAAGGAAATTGCTTTC
6068	Table 3A	Hs.167208	BE674762	10035230	7e98d05.x1 cDNA, 3' end /clone=IMAGE:3293193 /clone_end=3'	-1	AAATCAGGCCCTTGGCCATTCA AAAATCCTGTGAGATGACTCAAG
6069	db mining	Hs.283247	BE674807	10035275	7e93d11.x1 cDNA, 3' end /clone=IMAGE:3292725 /clone_end=3'	-1	AGGGCAGAGGTCCCTTGGGAGGGTA AGCTCACAAAACTCAGGGAGGCAG
6070	Table 3A	Hs.174010	BE674902	10035443	7e97a04.x1 cDNA, 3' end /clone=IMAGE:3293070 /clone_end=3'	-1	TCATCTCCGCCAAGGTTCCCACTAGG CAGGAAAGGATTTTATCTAAAGT
6071	Table 3A	Hs.174144	BE674951	10035492	7e97g10.x1 cDNA, 3' end /clone=IMAGE:3293154 /clone_end=3'	-1	CCACCCAAGTCCGAATCCGAGTGAA ATAAAATAGCATGCCCGCAACTAC
6072	Table 3A	Hs.190065	BE674954	10035505	7f11b09.x1 cDNA, 3' end /clone=IMAGE:3294329 /clone_end=3'	-1	AGGCACACGATTGTCACCAATTCTCC CTTACAAGCTGTATAATCAGTAA
6073	Table 3A	Hs.211828	BE675092	10035633	7f02d07.x1 cDNA, 3' end /clone=IMAGE:3293485 /clone_end=3'	-1	GCAACGTCTGAATGTAGTAATGTAC TCAGAGCTTCAAAGTAAGCATTG

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6074	db mining	Hs.330706	BE675125	10035666	IL3-UT0114-301100-357-H02 cDNA	-1	GCCACCCCATCTGGGAGGCCAGCA TCCAATTCACTGCCTTCATGATT
6075	db mining	Hs.283251	BE675180	10035721	7f03h06.x1 cDNA, 3' end /clone=IMAGE:3293627 /clone_end=3'	-1	TGATAGACTGGATGCTGCTATGGAA TCTGCCTCAGGAAAATGCCGGACT
6076	db mining	Hs.339281	BE675338	10035879	HNC29-1-D4.R cDNA	-1	TGGAGCCAAGAAGCCACTGACTCAA GAGGATTCAAGCGAGGCTGTTG
6077	db mining	Hs.283253	BE675379	10035920	7f08b02.x1 cDNA, 3' end /clone=IMAGE:3294027 /clone_end=3'	-1	CAACTTTGTAACAGGGGACTTAGCC GGGGCAGGAGGGGTTCTTGAGAC
6078	db mining	Hs.283254	BE675403	10035944	7f08d10.x1 cDNA, 3' end /clone=IMAGE:3294067 /clone_end=3'	-1	ACTTGAAAGGCACATCTTCTTTGGT TGTTTCCATCTCAAATTAAC
6079	db mining	Hs.283255	BE675434	10035975	7f09a10.x1 cDNA, 3' end /clone=IMAGE:3294138 /clone_end=3'	-1	TAAAAACTGACATGACATGAGATGGT TTAAGTGTCAAACATAAGGGCTTT
6080	db mining	Hs.283256	BE675531	10036072	7f10h08.x1 cDNA, 3' end /clone=IMAGE:3294303 /clone_end=3'	-1	ACTGACATAAGCCCACCTTCAGGTGTT TGGAAGACACTAAAGAGAACAGA
6081	db mining	Hs.315345	BE675610	10036151	7f12g09.x1 cDNA, 3' end /clone=IMAGE:3294496 /clone_end=3'	-1	GCAGCTTTTGCTGGCGGGGCTCA AATAAAGTAGCTCCCCAAAGAAA
6082	db mining	Hs.180637	BE675718	10036259	7f14h04.x1 cDNA, 3' end /clone=IMAGE:3294679 /clone_end=3'	-1	ACCTGGTTATCTCGCAATGACCTAGC TAACACAAATGCAACATCAGCCGG
6083	db mining	Hs.283258	BE675792	10036333	7f16b02.x1 cDNA, 3' end /clone=IMAGE:3294795 /clone_end=3'	-1	TGATCAAATGAAGATGCTCCAACCG TATAAATGGCAGATGAAATAGACT
6084	db mining	Hs.283259	BE675819	10036360	7f17d10.x1 cDNA, 3' end /clone=IMAGE:3294931 /clone_end=3'	-1	GCAGGAGAGAAAATACCTCTAAATGGG TGTGGACACTGGAGGAACGTGTTAC
6085	db mining	Hs.283261	BE675957	10036498	7f19b08.x1 cDNA, 3' end /clone=IMAGE:3295091 /clone_end=3'	-1	AGGGCACTGTTGTCCTTAATATG GAGAAATATGCAAATAACTGGGA
6086	db mining	NA	BE676019	10036560	7f20c12.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:3295222 3' similar to contains Alu repetitive element; m	-1	TTGGCCTATGTTAAATTCTATTCTAG TTCTTCTGTGCCCTTCCTCCCT
6087	Table 3A	Hs.170584	BE676049	10036590	7f21a03.x1 cDNA, 3' end /clone=IMAGE:3295276 /clone_end=3'	-1	GAACGTAAGCCCGACGCTAGGCAGT GCTGTAGAAAGTGTATTGGAAAGAG
6088	Table 3A	Hs.181015	BE676054	10036595	signal transducer and activator of transcription 6, interleukin-4 induced (STAT6), mRNA /cds=(165,2708)	-1	ATCCCATTCTCCCTCTCAAGGCAGGG GTCATAGATCCTAACGCCATAAAAT
6089	db mining	Hs.283263	BE676154	10036685	7f24a12.x1 cDNA, 3' end /clone=IMAGE:3295582 /clone_end=3'	-1	TGCTGTAAAATGGCAGCTCCATAGGA ACCTATTTCCATAGGAACCTGCA
6090	db mining	Hs.283264	BE676173	10036714	7f24c12.x1 cDNA, 3' end /clone=IMAGE:3295606 /clone_end=3'	-1	ACTGGAGAAAGGTGTCTTCCTGTCT TTCAGGGGCTCTGCGGGGAAATTC
6091	Table 3A	Hs.134648	BE676210	10036751	7f25c05.x1 cDNA, 3' end /clone=IMAGE:3295688 /clone_end=3'	-1	ATTATATTGTCCCTATCAGAACCTTC GAATCCCTAGCAGCCAGTCCCTG
6092	db mining	Hs.283266	BE676275	10036816	7f26d04.x1 cDNA, 3' end /clone=IMAGE:3295783 /clone_end=3'	-1	TGCTCACTGTCTCTGGAAGAGACAA GCACTTCTGAAATTCTAACAGCA
6093	Table 3A	Hs.158714	BE676408	10036949	7f29b11.x1 cDNA, 3' end /clone=IMAGE:3296061 /clone_end=3'	-1	CAATCGGATCATTCTCTCAACTTGG GCGGCTTTCCCTCCCTCCCTCC
6094	Table 3A	Hs.220929	BE676472	10037003	cDNA FLJ14369 fis, clone HEMBA1001174, highly similar to ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 5 /cds=(207,746)	-1	TGCTTGGGCAGTAGCTGAAGCCGA AGTATGAACAGTCCATTGTTCT
6095	db mining	Hs.283268	BE676474	10037005	7f30c08.x1 cDNA, 3' end /clone=IMAGE:3296174 /clone_end=3'	-1	CACAGTTGAGTAGGAGGTATGAAGA AGAAGAGATGATACCTGCCTTACC
6096	db mining	Hs.283269	BE676528	10037069	7f31d12.x1 cDNA, 3' end /clone=IMAGE:3296279 /clone_end=3'	-1	TTTGTGTAGCAAATGTTCTTAATTGC CTACTTGTGCCAAATTCAAGGCC
6097	Table 3A	Hs.123254	BE676541	10037082	AL572805 cDNA /clone=CSD01034YH06-(3-prime)	-1	TCCAGCATTGTTATTGTCTATTGACAC ACAAAGTTGAAAATAAGGGGCA
6098	db mining	Hs.283265	BE676548	10037089	7f79f01.x1 cDNA, 3' end /clone=IMAGE:2386969 /clone_end=3'	-1	CACCCACCAGACCGAGGATTCCAAAAA GGGGCGAAGCGGGAGAGCAAGG
6099	db mining	Hs.283270	BE676613	10037154	7f33a08.x1 cDNA, 3' end /clone=IMAGE:3296438 /clone_end=3'	-1	TGGACTCTGTTTCAAGAGGAAGAAA CAACTGACAAATAAGTTGATGTCA
6100	db mining	Hs.283271	BE676614	10037155	7f33a10.x1 cDNA, 3' end /clone=IMAGE:3296442 /clone_end=3'	-1	ATGTTGAAACTGGTTTAACTTGTAAAT GGTGTGGCTGATGTTACCCGACC
6101	db mining	Hs.283272	BE676667	10037208	7f34a07.x1 cDNA, 3' end /clone=IMAGE:3296532 /clone_end=3'	-1	ACACAGATTGAAAGTCACTGGCTA AATGGCCTCTACTTCCTGCTGTCA

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6102	db mining	Hs.102165	BE676737	10037278	7f37g03.x1 cDNA, 3' end /clone=IMAGE:3296884 /clone_end=3'	-1	GGAACCTTCTGCTTCACTTACGATGA AGAACATTGTACTCAATCCATCCA
6103	db mining	Hs.283276	BE676772	10037313	7f35d05.x1 cDNA, 3' end /clone=IMAGE:3296849 /clone_end=3'	-1	GAAGCCTTCCTGTGGTCATAACAAGT CTCACACACCCCAGGACTGTATCT
6104	db mining	Hs.86781	BE738569	10152561	601572850F1 cDNA, 5' end /clone=IMAGE:3838581 /clone_end=5'	-1	GAGTCAGCCTTGAACCTGGCGCT GAATCCTGACTTACTGCTTATTCA
6105	Table 3A	Hs.293842	BE748663	10162655	601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5'	-1	AAACTCATACATGCAGAAAATTGTCT TGCTGAAATGGTAATGCCAAA
6106	Table 3A	Hs.293842	BE748663	10162655	601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5'	-1	AAACTCATACATGCAGAAAATTGTCT TGCTGAAATGGTAATGCCAAA
6107	Table 3A	Hs.270293	BE857296	10371182	7g27b01.x1 cDNA, 3' end /clone=IMAGE:3307657 /clone_end=3'	-1	ACAAAAGTCATGGCTGTGAGGCTATC ATTACCCCTTTACCAAAGTTGGAA
6108	Table 3A	Hs.155935	BE858152	10373065	complement component 3a receptor 1 (C3AR1), mRNA /cds=(0,1448)	-1	AGTTCTATTTCTATCCCAAACTAAGCT ATGTGAAATAAGAGAAGCTACTTTGT
6109	Table 3A	Hs.294348	BE961923	11764299	601655335R1 cDNA, 3' end /clone=IMAGE:3845768 /clone_end=3'	-1	ATCCCGATGGTCCCCACCGCTATTAA AGGTTCTGTTGTTCCACGATTAAA
6110	Table 3A	Hs.5181	BE962588	11765636	proliferation-associated 2G4, 38kD (PA2G4), mRNA /cds=(97,1281)	-1	ATGTCTCCATACCCATTACAATCTCC AGCATTCCCTCAAAACCTAAAAA
6111	Table 3A	Hs.314941	BE962883	11766238	602381893F1 cDNA, 5' end /clone=IMAGE:4499447 /clone_end=5'	-1	GCCCGTATTACCCCTATAGCACCCCCC TCTACCCCCCTTAGAGCCCCAAA
6112	Table 3A	Hs.301110	BE963194	11766612	601656811R1 cDNA, 3' end /clone=IMAGE:3865731 /clone_end=3'	-1	ACATTTCTCCGCATAAGCCTGCGT CAGATTAACACTGAACTGACAA
6113	Table 3A	Hs.330887	BE963374	11766792	601657137R1 cDNA, 3' end /clone=IMAGE:3866193 /clone_end=3'	-1	CCAAGCTGGTTCAAGCCAACCCAT GGCCCTCATGACTTTTCCAAAAC
6114	Table 3A	Hs.334926	BE963551	11766970	Homo sapiens, clone MGC:8857 IMAGE:3866266, mRNA, complete cds /cds=(62,133)	-1	TGATCAGGTGAAACCGGAAGTCTCCAA TTTCTGAATGGATTATGTTCTAA
6115	Table 3A	Hs.316047	BE963666	11767085	601656685R1 cDNA, 3' end /clone=IMAGE:3866820 /clone_end=3'	-1	TGAGTACGTGACACTTGTGTTAGAAT AGTGGTGTGAGCTATATTCTGT
6116	Table 3A	Hs.294578	BE963811	11767228	601657462R1 cDNA, 3' end /clone=IMAGE:3875846 /clone_end=3'	-1	GTGACCCCTGGCACCCGCTAGAAGTT TATGGCCGAGCTTACCAATTAAA
6117	Table 3A	Hs.302585	BE964028	11767356	601657601R1 cDNA, 3' end /clone=IMAGE:3875617 /clone_end=3'	-1	TGAACCTCAAACTTGACCAACCCATG AGACCCCTGTTATCCAACTTCT
6118	db mining	Hs.210628	BE964051	11767519	601472729T1 cDNA, 3' end /clone=IMAGE:3875791 /clone_end=3'	-1	CCCTCTACTATTTGGCTCCATAACTTA GGACCTGCCTTCCCGGTTCCAG
6119	Table 3A	Hs.330588	BE964134	11767602	601151626F1 cDNA, 5' end /clone=IMAGE:3507774 /clone_end=5'	-1	CCCGTATTACCCATAGCACCCCCCT CTACCCCCCTTAGAGCCCCAAA
6120	Table 3A	Hs.252259	BE964149	11767617	ribosomal protein S3 (RPS3), mRNA /cds=(22,753)	-1	CCAACTTTCAGAACAGAAGGGGGG AAACCGAGAACCGGCTGCCATGCC
6121	Table 3A	Hs.184052	BE964596	11768078	PP1201 protein (PP1201), mRNA /cds=(75,1010)	-1	GCCCGAGAAATCCAATCCAGCCCCA GGATATAGTTAGGATTAATTACTTA
6122	Table 3A	Hs.286754	BE965319	11769559	601659229R1 cDNA, 3' end /clone=IMAGE:3895783 /clone_end=3'	-1	CTGAGATTTGGTTTCCACACCGGG CCAAGATACCCGGCTCTGCTGAG
6123	Table 3A	Hs.297180	BE965554	11770044	601659486R1 cDNA, 3' end /clone=IMAGE:3896204 /clone_end=3'	-1	ATATCATTCCACCTTAGTATTATACCC ACACCCACCCAAGAACAGGGTT
6124	Table 3A	Hs.108327	BF001438	10701713	damage-specific DNA binding protein 1 (127kD) (DDB1), mRNA /cds=(109,3531)	-1	ACAGCATGAGAAACTGTTAGTACGCA TACCTCAGTCAAACCTTCTGGGA
6125	Table 3A	Hs.161075	BF001821	10702096	7g93g02.x1 cDNA, 3' end /clone=IMAGE:3314066 /clone_end=3'	-1	GCTTGCCTAGCAGAGTCATACGGAA TAATGGAAAACCTAACCTCTGTTC
6126	Table 3A	NA	BF056055	10809951	7k07h12.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3443950 3' similar to contains element L1 repetitive elemen	-1	CACAATGCTGCCCTCTGTGGATGA CTGATGGCAAGAGTCGTGAATTGAA
6127	Table 3A	Hs.221695	BF058398	10812294	7k30d01.x1 cDNA, 3' end /clone=IMAGE:3476785 /clone_end=3'	-1	CCTCTCACTCTCAGACTCCAAGGGCC AAGAAAAACTACGGCAGGAAAGCC
6128	db mining	Hs.255684	BF058429	10812325	7k30g11.x1 cDNA, 3' end /clone=IMAGE:3476949 /clone_end=3'	-1	GAGAGGAGGGGTCTCAGACGTTGGG GGACACACTGCTGGGTGGTGATTT
6129	Table 3A	Hs.43857	BF058599	10812495	mRNA for KIAA1247 protein, partial cds /cds=(285,2942)	-1	TAAGAAATCCCAATTTCAGGAGTGG TTGTTGTCATAAAACGCTCTGTGGC
6130	Table 3A	Hs.144583	BF059133	10813029	Homo sapiens, clone IMAGE:3462401, mRNA, partial cds /cds=(0,153)	-1	CGGCAGGGTGGCTGTAAACATTCA GTTTCGCAGAACATTCAAGGTATT

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6131	db mining	Hs.257697	BF060727	10819637	AL533532 cDNA /clone=CS0DN004YJ14-(5'-prime)	-1	GGGGCTCCCTCCGGCTTGTGTTTC TCTGGAGATTTATTTACCTAA
6132	Table 3A	Hs.193237	BF062295	10821193	7k76b11.x1 cDNA, 3' end /clone=IMAGE:3481293 /clone_end=3'	-1	GAAAGTGGAGGGAGTGGACGGGGAG GAGACTAGCCAGAGAGGCTATTAG
6133	Table 3A	Hs.174215	BF062628	10821538	7h62b05.x1 cDNA, 3' end /clone=IMAGE:3320601 /clone_end=3'	-1	CTTCTCCCTTGCCTCTGGTC TGATTTAAAACGAAAAGGTGGAT
6134	db mining	Hs.159013	BF063675	10822585	hh82b10.x1 cDNA, 3' end /clone=IMAGE:2969275 /clone_end=3'	-1	GGACTCTGAAATAGAGCTGGCTCCC TGGGGTGACAATGTATATGCAA
6135	Table 3A	Hs.125887	BF109873	10939563	hypothetical protein FLJ14464 (FLJ14464), mRNA /cds=(69,3146)	-1	CTGGGTGTCGGAAGATGACGAAG ATGCTGGGCTGGCAGATGCAGTCCA
6136	Table 3A	Hs.288443	BF110312	10940002	7n36d08.x1 cDNA, 3' end /clone=IMAGE:3566654 /clone_end=3'	-1	ACCAGGGCTAAAACCTCAATTATTATG TTCATGACAGTGGGGATTTCCTT
6137	Table 3A	Hs.250905	BF116224	10985700	hypothetical protein (LOC51234), mRNA /cds=(0,551)	-1	ATTCTCCAACCACAAACAGCACTTCT AAAACTAACCTTACTTCTGCCCA
6138	Table 3A	Hs.318215	BF183507	11061818	601809991R1 cDNA, 3' end /clone=IMAGE:4040470 /clone_end=3'	-1	GATAATGCTCCATACCCCATACCA TCTCCAGCCATTCCCCCTCCAAC
6139	Table 3A	Hs.96566	BF194880	11081165	602137338F1 cDNA, 5' end /clone=IMAGE:4274048 /clone_end=5'	-1	TGATACTTGGTTCTTCTGCTCA GGTCCCTTCAATTGACTTTGGA
6140	Table 3A	Hs.232257	BF195579	11082811	RST2302 cDNA	-1	TAATACTGGAGGGCTTGAAGAAGG CTGTCGTGTTTGTACCTGCTTGT
6141	Table 3A	Hs.3353	BF197153	11085769	beta-1,3-glucuronidyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA /cds=(175,1179)	-1	GTCTTCCCGTCTTCTCTCACCTA TGTAATTTCAGTAGTCTCTCAGC
6142	Table 3A	NA	BF197762	11087169	7p9102.x1 NCI_CGAP_Skn1 cDNA clone IMAGE:3653139 3', mRNA sequence	-1	AGGAAGAGCCTGCACCTGTGGTGA ACAATCAGGAAAAGGAAGTCAAA
6143	Table 3A	Hs.50785	BF221780	11128957	SEC22, vesicle trafficking protein (S. cerevisiae)-like 1 (SEC22L1), mRNA /cds=(119,766)	-1	TTGGAGCTCTATAGGAGTGGAGAG GGGCAGCTCATTTGTTGAGAGTTGC
6144	Table 3A	Hs.250811	BF432643	11444806	v-ras simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB), mRNA /cds=(170,790)	-1	TGATCTGACTGGAAAACAATCTGTGA TCCCCTCCCAAAGAATCATGGGCT
6145	Table 3A	Hs.296356	BF433058	11445221	mRNA; cDNA DKFZp434M162 (from clone DKFZp434M162) /cds=UNKNOWN	-1	TCATCCCTTAAACACTCTGTGATGGG ATCTTCAGGATCATTTTGAAAGT
6146	Table 3A	Hs.76611	BF433353	11445516	601435773F1 cDNA, 5' end /clone=IMAGE:3920562 /clone_end=5'	-1	TGCGTTGGTTAGGAATGTGCTTT GTACTTCCACTTGAATAAAGGTGT
6147	Table 3A	Hs.178703	BF433657	11445846	AV716627 cDNA, 5' end /clone=DCBBCH05 /clone_end=5'	-1	TGCTCAGGGCACATGCACACAGACAT TTATCTGCACTCACATTGTTG
6148	Table 3A	Hs.222833	BF435098	11447386	7p05g01.x1 cDNA, 3' end /clone=IMAGE:3645097 /clone_end=3'	-1	GGTATTGCTGACACGCTGTCTCTG GCGACCTGCGCTGGAGAGGTGG
6149	Table 3A	Hs.293476	BF435621	11447923	hypothetical protein FKSG44 (FKSG44), mRNA /cds=(126,1520)	-1	CGTTTCTGAGCATCGTTGTGCCCT AACATTTCGCTGTCTTGGG
6150	db mining	Hs.257641	BF436704	11448943	7p07d12.x1 cDNA, 3' end /clone=IMAGE:3644999 /clone_end=3'	-1	CTTCTGAATGCCGAGTCTCTCTT TGTCCTCACAAATGCCACCCAAAC
6151	Table 3A	Hs.160980	BF437585	11449991	7p74d12.x1 cDNA, 3' end /clone=IMAGE:3651526 /clone_end=3'	-1	TGTTTACAAGGGTGATTGACCTTGCC TTACTCTTATGAAATTATGGCA
6152	db mining	Hs.258513	BF437915	11450432	AF150421 cDNA /clone=CBNBCG12	-1	CTGGCGTATTACCATTTGATAGCCT CTCTCAGGCTAGATAAGCTGGGG
6153	Table 3A	Hs.126594	BF445163	11510224	nad21d12.x1 cDNA, 3' end /clone=IMAGE:3366191 /clone_end=3'	-1	CCCTGTATTATTGAAATGTCAGCATA ATGACTGGAGGTGAAATTGGTCC
6154	Table 3A	Hs.174104	BF445405	11510543	601438710F1 cDNA, 5' end /clone=IMAGE:3923643 /clone_end=5'	-1	ACTGCTGTTGATGAATAGATGATAC AAAGCAAGTGTGAGGGTTGGTATG
6155	Table 3A	Hs.143389	BF446017	11511155	7p18a11.x1 cDNA, 3' end /clone=IMAGE:3646004 /clone_end=3'	-1	TGGAAGAACAAATTGAGACATCATCA GTAAGTCTTAGGGACACAGGGA
6156	Table 3A	Hs.295726	BF447885	11513023	integrin, alpha V (vitronectin receptor, alpha polypeptide antigen CD51) (ITGAV), mRNA /cds=(41,3187)	-1	AGTGAAGAACTGGTACAGTGTCTGCT TGATTTACACATGTAACCTGTGA
6157	Table 3A	Hs.179526	BF475501	11546328	upregulated by 1,25-dihydroxyvitamin D3 (VDUP1), mRNA /cds=(221,1396)	-1	GCCAGAAAGTGTGGGCTGAAGATGG TTGGTTCATGTTTTGTATTATGT
6158	Table 3A	Hs.181311	BF478238	11549065	asparaginyl-RNA synthetase (NARS), mRNA /cds=(73,1719)	-1	TGTCCTCTGAACCTGAGTGAAGAAAT ATACTCTGCTCTTGTACCTCGCT
6159	Table 3A	Hs.179703	BF507849	11591147	tripartite motif protein 14 (TRIM14), mRNA /cds=(10,1230)	-1	CCATTTCACATCATGCCCTCCTAC CTTCCCTTCACAACCAATCAACTG
6160	Table 3A	Hs.159673	BF508053	11591351	Ui-H-B14-apx-b11-0-Uls1 cDNA, 3' end /clone=IMAGE:3088845 /clone_end=3'	-1	ACACTCCCTGAATGTTGAAGAAGAT ATGCTATCCATGCAATCCCTTGTCG

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6161	Table 3A	Hs.158999	BF508694	11591992	UI-H-BI4-aop-f-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3085601 /clone_end=3'	-1	ACTTGTGTTGAACCACTTCGCTTC CTCTTAAACCTGAGATGCACACGT
6162	Table 3A	Hs.77542	BF508702	11592000	602629438F1 cDNA, 5' end /clone=IMAGE:4754432 /clone_end=5'	-1	ACATTCTCTCATTTCGCTGAAGCTGAT TTGATTGGGTGCTGTTCTCCG
6163	Table 3A	Hs.127311	BF508731	11592029	AU185774 cDNA /clone=B02302-013	-1	TGACAGAATGAACCTGAAATGAAATC CCACAGTTATGATCGTAGTAGAGT
6164	Table 3A	Hs.144265	BF509758	11593056	UI-H-BI4-apg-d-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3087390 /clone_end=3'	-1	AACTACAGATGCATCCCGTGCTGT GATCTCCAGGCCATTCTCCATTTC
6165	Table 3A	Hs.256931	BF510393	11593691	zb02d05.s1 cDNA, 3' end /clone=IMAGE:300873 /clone_end=3'	-1	ACTGCCAATCTGATTAAAATCTCCA AGCTTAATTCTGTCAACAAACCA
6166	Table 3A	Hs.276341	BF510670	11593968	UI-H-BI4-aof-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:3084615 /clone_end=3'	-1	GCTCTGGTTCTGTTTATGCCCTAT TTTACAAAATGATTCTGACCTGG
6167	Table 3A	Hs.248689	BF512500	11597602	UI-H-BI3-alw-h-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069162 /clone_end=3'	-1	AACTGGCATTGCTAAGCCCCAGAAAA ATGTATTAGTGGAACAGATGAAA
6168	Table 3A	Hs.136375	BF513274	11598453	602544150F1 cDNA, 5' end /clone=IMAGE:4666332 /clone_end=5'	-1	ACACTAGGCCTTTATACCTGTGCC TTTACGTTCGTTTCGATTGCA
6169	Table 3A	Hs.300870	BF513602	11598781	mRNA; cDNA DKFZp547M072 (from clone DKFZp547M072) /cds=UNKNOWN	-1	AATACAGATTCACTTATTAAGCGTC CGTGGCACCGACAGGGACCCAG
6170	Table 3A	Hs.255340	BF514247	11599426	UI-H-BW1-ani-h-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082601 /clone_end=3'	-1	AGTCATCCCCTTCAGAACAGCTGTT GCTCTGGCTCATAAACCTGTGA
6171	Table 3A	Hs.283022	BF514341	11599520	triggering receptor expressed on myeloid cells 1 (TREM1), mRNA /cds=(47,751)	-1	GCCTCTTTCCCTGATCACACAAGGG TCAGGGATGGTGGAGTAAAGCTC
6172	Table 3A	Hs.83734	BF515538	11600717	syntaxin 4A (placental) (STX4A), mRNA /cds=(66,959)	-1	TGTTAGGTGGCCCTCTGCATACCTATG GGAACTCAGTGATGTAATGCAAG
6173	Table 3A	Hs.146065	BF591040	11683364	AL580165 cDNA /clone=CS0DJ005YB18-(3-prime)	-1	CTGGGGCCGTAGCAAAATACTATGAAA AACACTTCAACGTGTCTTCAAT
6174	Table 3A	Hs.30941	BF592138	11684462	calcium channel, voltage-dependent, beta 2 subunit (CACNB2), mRNA /cds=(501,2318)	-1	TGCCAAGTCAGCAGATTGCTTATG AATTACAGGGACTAGAAATGCCCA
6175	Table 3A	Hs.695	BF690338	11975746	cystatin B (stein B) (CSTB), mRNA /cds=(96,392)	-1	TTGCATGTCTCTTCAAATTTCATTG TGTTGATTCTAACTCTCCCGT
6176	Table 3A	Hs.142838	BF732404	12057407	nucleolar protein interacting with the FHA domain of pK-67 (NIFK), mRNA /cds=(54,935)	-1	AGAGTGAGAAGGCAGTTCCAGTTA GCACAGATTGTTATGTGTTCAAG
6177	Table 3A	Hs.296317	BF938959	12356279	mRNA for KIAA1789 protein, partial cds /cds=(3466,4899)	-1	GAAGTGACACTGACTGTATCACCTC TCCTTTCTTCATCAGGTGTTCT
6178	Table 3A	Hs.182937	BF939014	12356334	peptidylprolyl isomerase A (cyclophilin A) (PP1A), mRNA /cds=(44,541)	-1	TCCCTGGGTGATACCATTCATGTTCT TAATGTAATTGCTGAGACCTG
6179	Table 3A	Hs.26136	BF940103	12357423	hypothetical protein MGC14156 (MGC14156), mRNA /cds=(82,426)	-1	AATTCCAAAGGAGTGTGTTGGAATA GTCCCTCTAAAGGAGAGAAATGCA
6180	Table 3A	Hs.133372	BF940291	12357611	AF150127 cDNA /clone=CBCBGA01	-1	AGCCCCCTCCACCCACCCAGTACTTT TAAATGTTATTAAAGACCCCT
6181	Table 3A	Hs.304900	BF980139	12347354	602288147F1 cDNA, 5' end /clone=IMAGE:4373963 /clone_end=5'	-1	CCATCCTTGAGAAATGTGGCACCAA GTCCATAATCTCCATAAAATCCAAT
6182	Table 3A	Hs.303214	BG054649	12511436	7c45b01.x1 cDNA, 3' end /clone=IMAGE:3576912 /clone_end=3'	-1	CGTTGCATTTCACATTGTGTTGGCA GGACAAGCATGGGGCAAGAGGGAC
6183	Table 3A	Hs.8258	BG054866	12512220	cDNA FLJ14737 fis, clone NT2RP3002273, weakly similar to SCD6 PROTEIN /cds=(77,1468)	-1	TATGAGTTATGCGTTTCCAGCCC TCCGAATCACTGACTGGGGCGTT
6184	Table 3A	Hs.179661	BG056668	12521375	Homo sapiens, tubulin, beta 5, clone MGC:4029 IMAGE:3617988, mRNA, complete cds /cds=(1705,3039)	-1	TTGAAAAGATGACATGCCCAAGAG CCAAAATAATGGGAATTGAAAA
6185	Table 3A	Hs.56205	BG057282	12522612	insulin induced gene 1 (INSIG1), mRNA /cds=(414,1247)	-1	TGCACTCTACCAGATTGAACATCTA GTGAGGTTACATTCTACTAACT
6186	Table 3A	Hs.3709	BG057892	12523835	low molecular mass ubiquinone-binding protein (9.5kD) (QP-C), mRNA /cds=(77,358)	-1	TGGTGTATCTGCTTAGATTCCCTG TATCTTGCTGCCCTCTTCAGT
6187	Table 3A	Hs.5122	BG058599	12525258	602293015F1 cDNA, 5' end /clone=IMAGE:4387778 /clone_end=5'	-1	AGTTGGAGCTATCTGTCAGCAGTT CTCTACAGTTGTCATAATGTTT
6188	Table 3A	Hs.89104	BG058739	12525527	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	CGTGGGAGGATGACAAAGAACATG AGTCACCCCTGCTGGATAAACTTAA
6189	Table 3A	Hs.166982	BG149747	12661777	phosphatidylinositol glycan, class F (PIGF), mRNA /cds=(67,726)	-1	GTTGTTGGTCAGCATAACACACTCT CATTTCATTGATGTACACAGCCA
6190	Table 3A	Hs.100293	BG149986	12662016	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) (OGT), mRNA /cds=(2039,4801)	-1	ACCTGGGATTTCATTCTGCTGAAAG AAATAGGAAGAACAGGACTCACTT

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6191	Table 3A	Hs.198427	BG150273	12662303	hexokinase 2 (HK2), mRNA /cds=(1490,4243)	-1	GGGTGTGATGAATAGCGAATCATCTC AAATCCTTGGCACTCAGTCAGT
6192	Table 3A	Hs.313610	BG150461	12662491	7k01d08.x1 cDNA, 3' end /clone=IMAGE:3443006 /clone_end=3'	-1	AGCTTCACCACCTCGCAGTTGAGA GATAGTCCCCGAAATATTATCCCA
6193	Table 3A	Hs.184456	BG230563	12725596	hypothetical protein (LOC51249), mRNA /cds=(0,611)	-1	GTGTGAAGTGACAGCCTGTGTGA TGTCTCTGCCCTCCCAAGTTG
6194	Table 3A	Hs.89104	BG231557	12726684	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	TGTTTTAACAACTCTCTCAACATTT TGCCAGGTTTACTGTAAACCA
6195	Table 3A	Hs.152925	BG231805	12726934	mRNA for KIAA1268 protein, partial cds /cds=(0,3071)	-1	TAAGTGGATTGGCAGACTCCTTGTG CTTAAAGAGTGCCCTTAGGCAGG
6196	Table 3A	Hs.89104	BG231961	12727100	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	TTGTTTTAACAACTCTCTCAACATTT TGCCAGGTTTACTGTAAACCA
6197	Table 3A	Hs.337986	BG235942	12749789	Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336,1494)	-1	GCCAGTCTCTATGTGCTTAATCCCT TGTCTTCATTAAGCAAAACTA
6198	Table 3A	Hs.3353	BG236015	12749862	beta-1,3-glucuronidyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA /cds=(175,1179)	-1	GTCCTTCCCGCTTCTCTCACCTA TGAAATTTCAGTAGTCTCAGC
6199	Table 3A	Hs.75703	BG236084	12749931	small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386)	-1	GGTCACTCTCACTCTCTGCTG TTGCAAATACATGGATAACACCGT
6200	db mining	Hs.5146	D19756	500072	HUMGS00712 cDNA, 3' end /clone=mm0970 /clone_end=3'	-1	CATTCAGTATTTATTGGGAAGACTTG TCAAGCACCATGATAAGTGGTGA
6201	db mining	Hs.237971	D19770	500086	hypothetical protein MGC5627 (MGC5627), mRNA /cds=(72,584)	-1	AGAGGGGAAGGACTTACATGACAT CCTACTGGGAATTGCTAGAAACCA
6202	db mining	Hs.30709	D20225	501322	HUMGS01199 cDNA, 3' end /clone=pm0880 /clone_end=3'	-1	CTGGTGAAGCTGACTCCCCAGTAAA GAGATATCAGCTCTGCTTCAGACT
6203	db mining	Hs.30731	D20378	501474	HUMGS01352 cDNA 3' end /clone=pm2843 /clone_end=3'	-1	TTGCTTCTCCCTGCTTTAGAGTTCC CGTAAATAACCCCTCACCCCTGGC
6204	db mining	NA	D20425	501521	HUMGS01399 Human promyelocyte cDNA clone pm1281 3', mRNA sequence	-1	TCTGACCTCCGTGACGTTTATTACCA GCTGATGTCCCGTACACTGATTCA
6205	db mining	Hs.228071	D20458	501554	HUMGS01432 cDNA, 3' end /clone=pm1542 /clone_end=3'	-1	GGGAAGGGTCAGCAACGATTTCTCA CCAATCACTACACAGACACAAAGG
6206	db mining	Hs.330221	D20465	501561	HUMGS01439 cDNA, 3' end /clone=pm2194 /clone_end=3'	-1	ACCACTAAATGGTTACACTACACCAA GACACTAAATGGCAGGGAGCCT
6207	db mining	Hs.92440	D20522	501618	HUMGS01497 cDNA, 3' end /clone=pm1507 /clone_end=3'	-1	AAATTCAAATCACCCCTGATAACCCAC TTCCTTCTCCACCCAAATCTGAT
6208	db mining	Hs.90165	D20538	501634	HUMGS01513 cDNA, 3' end /clone=pm1504 /clone_end=3'	-1	ACCATATCGTGCACAAATGTAATATGG AATTCCAACATCAATGAAGGAT
6209	db mining	Hs.90171	D20572	501668	HUMGS01547 cDNA, 3' end /clone=pm1503 /clone_end=3'	-1	AATAAGTACCGTATAAACACTTCTC TTCTCTCCACCAATGGCAAG
6210	db mining	Hs.30766	D20726	504546	HUMGS01703 cDNA, 3' end /clone=mp0684 /clone_end=3'	-1	AGCATCACTCTAGAAGAAGCAACTC CTCCCTGATTCTGTGATTGG
6211	db mining	Hs.5816	D20846	504666	HUMGS01827 cDNA, 3' end /clone=mp0825 /clone_end=3'	-1	TCAACCAGAACATCTATAATGTATGAA ATAAAATTAAATAGAGAACCCAAACAGATC
6212	db mining	Hs.30793	D20888	504708	HUMGS01869 cDNA, 3' end /clone=mp0836 /clone_end=3'	-1	AAGGTCTCATCTAACAGGTAGAGCA GTTGGTGCAGATGAGATGAGCTG
6213	Table 3A	Hs.292590	D59502	960608	602626586F1 cDNA, 5' end /clone=IMAGE:4751396 /clone_end=5'	-1	GGTGTGATACCAACCTCCAATGAA GGGAAGCAAGTTCATCAGTCACA
6214	Table 3A	Hs.119274	F13765	758015	RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4-binding protein) (GAP1IP4BP), mRNA /cds=(46,2550)	-1	AGCTGTTGGGGCTGCACTGAGCTGC AATTTTAACATGGATTATAACTT
6215	db mining	Hs.238797	H07915	872737	602081661F1 cDNA, 5' end /clone=IMAGE:4245999 /clone_end=5'	-1	AAGGAATTGTTTCCCTATCTTAAC CAGTAACAGAGGGTTTACTCCGA
6216	db mining	Hs.11307	H09541	874363	RST29274 cDNA	-1	CGCACACATTTCTGTATGGACAAAT CCTGGATTGGCTCGTTATTGGT
6217	Table 3A	Hs.187908	H69141	1030426	EST375312 cDNA	-1	GGTAATGAAACATCATCCAGTTAAC AATCAGCAAGGTTCTTCAGAGCCT
6218	Table 3A	Hs.117005	H71238	1043052	sialic acid binding Ig-like lectin 5 (SIGLEC5), mRNA /cds=(142,1797)	-1	TGGAAGAGTGGACTGAAGAAAGAACT TATACTCTCCCTCTAAATGAA
6219	Table 3A	NA	H78395	1056484	yu12f03.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:233597 3' similar to contains Alu repeat	-1	TCCGGCTATGGCTTATGATATC TTTTGAGAAACAGGATTTCACCTT
6220	Table 3A	Hs.38664	H80108	1058197	ILO-MT0152-061100-501-e04 cDNA	-1	ACCTTTAAGGATGTCTTATTCACC CCAACCTCTCCACTCCATTAGT
6221	Table 3A	NA	H92914	1099242	yt94g03.s1 Soares_pineal_gland_N3HPG cDNA clone IMAGE:231988 3', mRNA sequence	-1	GAACCTTCAAAACTGTCACTTGTGAGT TCCAGAAGAGTCCCTCACCATCTT
6222	Table 3A	Hs.2210	L40410	703109	thyroid receptor interactor (TRIP3) mRNA, 3' end of cds /cds=(0,458)	-1	GTATTTGGCTTCTCCAAGCAGATCA CGCAGACGACGGTGTACATTGA
6223	Table 3A	Hs.2200	L40557	705359	perforin 1 (preforming protein) (PRF1), mRNA /cds=(0,1667)	-1	CAAGCATACTGGTTCTTCAAGCTC ACTGTTCTCACACACGGCCCCAC

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6224	Table 3A	Hs.198726	M24069	181483	vasoactive intestinal peptide receptor 1 (VIPR1), mRNA /cds=(56,1543)	-1	TCCATATCCATTCTGACGTGAACC ATTGGACAGTGCAAGGACTTTGG
6225	Table 3A	Hs.132911	N20190	1125145	MR2-OT0079-290500-007-b03 cDNA	-1	AAGCTGTTTCACTCTAAAAATTCA AGAGGACACGCTAAAGAACGATCA
6226	Table 3A	Hs.323950	N23307	1137457	zinc finger protein 6 (CMPX1) (ZNF6), mRNA /cds=(1265,3381)	-1	CCTCAGCTTCCAACCTCTGATTCAGG ACAGGATGAAAACCTTGGACAG
6227	Table 3A	Hs.32250	N30152	1148672	yx81f03.s1 cDNA, 3' end /clone=IMAGE:268157 /clone_end=3'	-1	GCGCACATGGCTATTGTGATAACAA AGTTGTGTTGCTACTTTAGAACG
6228	db mining	Hs.44512	N33584	1153983	yv21f11.s1 cDNA, 3' end /clone=IMAGE:243405 /clone_end=3'	-1	AACTCACGACAATTGCTACAAACAC CAGGGAGGGGCTTTTGTGTTTT
6229	Table 3A	Hs.3353	N36787	1157929	beta-1,3-glucuronidyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA /cds=(175,1179)	-1	GCTTATCCCCTCTTCTCCTCACCTA TGTATTTCAGTAGCTCTCACGC
6230	Table 3A	Hs.38218	N39230	1162437	602569369F1 cDNA, 5' end /clone=IMAGE:4693744 /clone_end=5'	-1	GCCCTGGTATGTATGCCCTTCTCTCC TACTGTCTAAAGCACCTCGTAA
6231	Table 3A	Hs.236456	N49836	1191002	602287746T1 cDNA, 3' end /clone=IMAGE:4375057 /clone_end=3'	-1	AAGAAACCGTGGAAAGATACTGGTTA TTTCAAATGAGCAGAGTATGTTG
6232	Table 3A	Hs.114453	N58052	1201942	601880526F1 cDNA, 5' end /clone=IMAGE:4109119 /clone_end=5'	-1	CCACCTCTCTGACATGAATGTAGCA TAAGTTAGCAATCGGTTCTCAA
6233	Table 3A	Hs.334731	N58136	1202026	Homo sapiens, clone IMAGE:3448306, mRNA, partial cds /cds=(0,2353)	-1	AGGTTCCCCTTCAAATAAGATAAAG AATTGACTTGGGACACTGCCAGA
6234	Table 3A	Hs.205555	N72600	1229704	za46f08.r1 cDNA, 5' end /clone=IMAGE:295623 /clone_end=5'	-1	GGCTGGCCTCATTTGAAAAGTTAGT ACAATTTCCTCAGTGCTAACCTTG
6235	Table 3A	Hs.256931	N80578	1243279	zb02d05.s1 cDNA, 3' end /clone=IMAGE:300873 /clone_end=3'	-1	ACTCCAGAACGTCAGAAATGGTGTAG CAGAAATGAATTCTGTATAAGGAA
6236	Table 3A	Hs.303018	N94511	1266820	zb80g04.s1 cDNA, 3' end /clone=IMAGE:309942 /clone_end=3'	-1	CTGTCGAAAGTTGGAGACTGCCGT ACCCAGGTTGATAGTCATTGTT
6237	db mining	Hs.118984	NM_017660	8923093	hypothetical protein FLJ20085 (FLJ20085), mRNA /cds=(62,655)	-1	CCACCTTGAGGCCCTTCTCTGGTTG GTTGTATGCAGTTCTCACACATG
6238	Table 3A	Hs.11594	R12665	765741	yf40a04.s1 cDNA, 3' end /clone=IMAGE:129294 /clone_end=3'	-1	ACCCTTCCCTTTTATATCCTTCT TCAAAAATCTAAATGATGTGCT
6239	db mining	Hs.108082	R40823	821181	60206898F1 cDNA, 5' end /clone=IMAGE:4067972 /clone_end=5'	-1	AGTCCAGGAGGTGGTTAAATATT GGATGAAAATCACAGGCTTTTT
6240	db mining	Hs.94881	R50838	812740	602387586F1 cDNA, 5' end /clone=IMAGE:4516388 /clone_end=5'	-1	ACAATACATTACAAGCCATTTAC ATGCATTAACGAGGGCTACAC
6241	Table 3A	Hs.94881	R50838	812740	602387586F1 cDNA, 5' end /clone=IMAGE:4516388 /clone_end=5'	-1	ACAATACATTACAAGCCATTTAC ATGCATTAACGAGGGCTACAC
6242	RG housekeeping genes	Hs.92004	R52541	814443	HSU55987 cDNA /clone=39883	-1	GGCCTGAAGAAGGGAGATAAGTGTTC CATTGGCAACATAAGAGAAAGTTAA
6243	RG housekeeping genes	Hs.26766	R60313	831008	602270716F1 cDNA, 5' end /clone=IMAGE:4359027 /clone_end=5'	-1	TCCATCCCAAAGGAGAGCTACTGTAC TGACTGTACTTGTGGAATGCAGCG
6244	db mining	Hs.330530	T25714	563034	ESTDIR309 cDNA, 3' end /clone=CDDIR9 /clone_end=3'	-1	ACCCACCACTCTCAGGACCACCTGAA GGCAGAATAAACCGGATCCTGTTG
6245	db mining	NA	T25727	563047	ESTDIRX51 CD34+DIRECTIONAL cDNA clone CDDIRX51 3', mRNA sequence	-1	AAATTGTGTGAGAAGGCTGATAAACG TCTGTGGTTCTCCCTGTGCTATT
6246	db mining	Hs.7569	T26893	567784	ESTDIR465 cDNA, 3' end /clone=CDDIR465 /clone_end=3'	-1	GCTGGGCTTCTGCAAAATTATAAAGT TGCTTATTAAATTCTACATGCGG
6247	db mining	Hs.172822	T26903	567794	ESTDIR551 cDNA, 3' end /clone=CDDIR551 /clone_end=3'	-1	AGCTGATTCTTCTATGTGTGC CACTAAATAAAGAGATTTGAGCAAGT
6248	Table 3A	Hs.185675	T98171	747516	QV2-EN0098-010201-603-a05 cDNA	-1	CTTGAAGCTGTGTTGGTGGCTGTGA CCTTCCAATGCAATCTAGACTGTG
6249	Table 3A	Hs.58066	W72392	1382348	602389077F1 cDNA, 5' end /clone=IMAGE:4517875 /clone_end=5'	-1	CTCATACACTCTCAGCCTCAGCACC TAACCCCTCACACAACTCCAGTA
6250	Table 3A	NA	W86427	1400194	zh61c11.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:416564 3', mRNA sequence	-1	TGAGTATTGTGTGGGGGGGGTAT GTCTGTATATAATCTGTGAGCCA
6251	Table 1	NA	AA136584	1697794	zn95b02.s1 Stragene fetal retina 937202 cDNA clone IMAGE:565899 3', mRNA sequence	-1	AACATATCCAGGGAGGACAACTCTG GGCTGGACAATGTATCCACAAAGGG
6252	Table 1	NA	AA431959	2115667	zw77a03.s1 Soares_testis_NHT cDNA clone IMAGE:782188 3', mRNA sequence	-1	AGAGCAAGTCTCAGAAATAATGCTGT ATCTACACTGTCTATGTTGCCA
6253	Table 1	NA	AA482019	2209697	zu98e04.s1 NCI_CGAP_GCB1 cDNA clone IMAGE:746046 3', mRNA sequence	-1	ACCAACAGCTTTGTAAATTCTCTCTT CTAAGGCATAGTGAACAACTTGCT
6254	Table 1	NA	AA524720	2265648	ng42e03.s1 NCI_CGAP_Co3 cDNA clone IMAGE:937468 3', mRNA sequence	-1	GGACGGTGGCTGAATGGCAACAGT GATGGAATATTATTTAGGCCACA

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6255	Table 1	Hs.57787	AA588755	2402486	602381381F1 cDNA, 5' end /clone=IMAGE:4498845 /clone_end=5'	-1	AGGTTGTTATCAGGTGGCACAAATTAA AATCCATCTTGAAGACTTCACACA
6256	Table 1	NA	AA628833	2541220	af37g04.s1 Soares_total_fetus_Nb2HF8_9w cDNA clone IMAGE:1033878 3', mRNA sequence	-1	GACTCGTTACGCCGTAGTTGTCCTA TCTTGTTATCAAATGAATTTCGTT
6257	Table 2	Hs.180669	AA633203	2555617	OS-4 protein (OS-4) mRNA, complete cds /cds=(305,1156)	-1	AGAGCTATGGGTGCTACAGGCTTGTC TTCTAAAGTGACATAATTCTTATCT
6258	Table 1	Hs.239489	AA639796	2563575	TIA1 cytotoxic granule-associated RNA-binding protein (TIA1), transcript variant 2, mRNA /cds=(185,1345)	-1	ACCTTATAAACAGAGCCCAGGAAA GACAGCTCGAGTGATAATTCTCT
6259	Table 1	Hs.29282	AA748714	2788672	mitogen-activated protein kinase kinase kinase 3 (MAP3K3), mRNA /cds=(83,1963)	-1	AGCTCCCTCCCTCTCAACACCCAGTTT CCTTGGGAGTTGTCACTAAAGGAA
6260	Table 1	Hs.111554	AA806222	2874972	ADP-ribosylation factor-like 7 (ARL7), mRNA /cds=(14,592)	-1	GCTGTAATTCTCTGTCTCATCATCCTT CTCTTTGTTCCATAGCCTTTT
6261	Table 1	NA	AA806766	2875516	ab91d04.x1 NCI_CGAP_GCB1 cDNA clone IMAGE:1338727 3', mRNA sequence	-1	TCGCTTCTAACTGATTCCATTCCAC CATGTCAGATACTCCTGGGCTGCT
6262	Table 1	Hs.226755	AA909983	3049273	RC1-UT0033-250800-022-h02 cDNA	-1	ATCCAAGCTTTAATTCTGCCATCTCA GAATGGTGTATAACCATTCTCCC
6263	Table 1	Hs.50252	AA984245	3162770	mitochondrial ribosomal protein L32 (MRPL32), mRNA /cds=(46,612)	-1	TCAGCCAAACCTGAATCTGTATCTTT ACTTAAACACAGCAGTTGAGTTA
6264	Table 1	Hs.53542	AI084224	3422647	chorea-acanthocytosis (CHAC) mRNA, complete cds /cds=(260,9784)	-1	TCAATAGTTGTAAATTCTTCTCAGG CTCCTTAAACCTCGCTTGTGTT
6265	Table 1	Hs.135187	AI091533	3430592	AV712378 cDNA, 5' end /clone=DCAAND12 /clone_end=5'	-1	AGAGGCAACACTAAACACTAGGGCT ACTGTGGCATCTATGTAGACAGGA
6266	Table 1	Hs.11637	AI275205	3897479	602388093F1 cDNA, 5' end /clone=IMAGE:4517086 /clone_end=5'	-1	TGACTTTCAAGGAATGTCACTTGAC CTCTCCTGCCACTGTTACTCAGC
6267	Table 1	Hs.8724	AI298509	3958245	serine threonine protein kinase (NDR), mRNA /cds=(595,1992)	-1	TCTCAAGAGAGAACGCCACAGCAGA GAGACCCAACTCCGCTTAAGTGCAG
6268	Table 1	Hs.142838	AI299573	3959158	nucleolar protein interacting with the FHA domain of pKi-67 (NIFK), mRNA /cds=(54,935)	-1	AGAGTGAAGGCAGTCCAGTTTA GCACAGATTGTTATGTGTTCAAG
6269	Table 1	Hs.100555	AI352690	4089896	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myo-regulated) (DDX18), mRNA /cds=(71,2083)	-1	GGGGTAGGAAGAGGATGGAATTGAG ATGTTGAGCCTCATTAACATCAAT
6270	Table 1	Hs.108124	AI362793	4114414	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	-1	GCTCGCTACCAGAAATCCTACCGATA AGCCCATCTGACTC AAAACTCAC
6271	Table 1	Hs.134342	AI363001	4114622	mRNA for LanC-like protein 2 (lanct2 gene) /cds=(186,1538)	-1	GAGCGCAGCACACCC TTGAGTGACAG CGACCTCTCTCTACAGGTTTCCC
6272	Table 1	Hs.192427	AI380016	4189869	602296277F1 cDNA, 5' end /clone=IMAGE:4390770 /clone_end=5'	-1	ACTTCCCCTTAGGTATCCCTGGAGT AATAATGACAACAAAATTCACTGCA
6273	Table 2	Hs.158976	AI380390	4190243	UI-H-BI2-ahi-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2726692 /clone_end=3'	-1	GTCCTTGTAGCAGAACAAAGGGCT CTGTGATCCTCTGGACCTCAGATT
6274	Table 1	NA	AI392705	4222252	tg23b03.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2109581 3', mRNA sequence	-1	TGCAGGCTCATTGTGCTCCTTCTCT GGGTTCAATTGGATTTCAGTCCT
6275	Table 1	Hs.76239	AI393970	4223517	hypothetical protein FLJ20608 (FLJ20608), mRNA /cds=(61,680)	-1	GAGGACTGGGACCGTGATTCCACTA ACCGGAAACCGTCCGCTTCCGGGCC
6276	Table 1	Hs.79968	AI419082	4265013	splicing factor 30, survival of motor neuron-related (SPF30), mRNA /cds=(0,716)	-1	GGATGTGTATGTTATATGGGAGAA CAAAAAGCTGATGTATAGCCCTGT
6277	Table 1	Hs.121973	AI458739	4311318	602428025F1 cDNA, 5' end /clone=IMAGE:4547239 /clone_end=5'	-1	CCTGAAACAGCTAACGCCAACAGGCA ACTTACCGTGGACTCAAACACTTGT
6278	Table 1	Hs.342008	AI498316	4390298	UI-H-BI1-aeq-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2720186 /clone_end=3'	-1	GCCAGAATGGTACAGAGTGGAGGGT GTTCTGCTAATGACTTCAGAGAAGT
6279	Table 1	Hs.194054	AI523854	4437989	HA0689 cDNA	-1	GACAAAATAGTTACCTATGCTTCCCT CTGGCACCCGAATGTAACGCAGG
6280	Table 1	Hs.14623	AI571519	4534893	Interferon, gamma-inducible protein 30 (IFI30), mRNA /cds=(40,951)	-1	AAGCCCAGATACACAAAATTCCACCC CATGATCAAGAATCTGCTCCACT
6281	Table 1	Hs.278554	AI627495	4664295	chromobox homolog 3 (Drosophila HP1 gamma) (CBX3), mRNA /cds=(111,662)	-1	TGCTGAAAGTGGTCCCAAAGGGGTA CTAGTTTTAAGCTCCCAACTCCCC
6282	Table 1	Hs.17132	AI633798	4685128	60236676F1 cDNA, 5' end /clone=IMAGE:4427970 /clone_end=5'	-1	GCAACTGTTCTAGGACATGTTAC TAGAACTACTTAAAGTATGCTGTGTC
6283	Table 1	Hs.4283	AI651212	4735191	602621616F1 cDNA, 5' end /clone=IMAGE:4755315 /clone_end=5'	-1	ACAGTTACTTGGAGCTGCTAGACTG GTTTCTGTGTTGTTAAATTGCT
6284	Table 1	Hs.324507	AI678099	4888281	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(182,2056)	-1	CGCCAGAGGTAGAACATGTCATT TGAATTGGATCGTTACAAATGAGC
6285	Table 1	Hs.90744	AI684022	4895316	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA /cds=(0,1268)	-1	TTCTGACGATTACACAACGAGGCT TTAATGCCATTGGGTAGGTGAGC

Table 8

6286	Table 1	NA	AI688560	4899854	wd39f08.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2330535 3', mRNA sequence	-1	ACTGAAAAGTTGAAAGACTTTGCAG TGAACATTTATAACTCCCGCT
6287	Table 1	Hs.177708	AI697756	4985658	602369210F1 cDNA, 5' end /clone=IMAGE:4477370 /clone_end=5'	-1	TGGTTCCTGTGCTCACCATAGGGCTG GTGTACATTGGGCCATTAAAC
6288	Table 1	Hs.80887	AI701165	4989065	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA /cds=(287,1835)	-1	TCTGGAAAGACATTTAAGCTGCT GACTTCACCTGCAAATCTAACAG
6289	Table 1	Hs.299883	AI742850	5111138	hypothetical protein FLJ23399 (FLJ23399), mRNA /cds=(282,1769)	-1	TGTTTACCTCACTGTTGGACATACAT TCCAAGCTTCACTCTAGGAG
6290	Table 1	Hs.14373	AI760353	5176020	yx26h11.r1 cDNA, 5' end /clone=IMAGE:262917 /clone_end=5'	-1	TTTATCTCAGAACTTGTGAACTCTG AAATGACCCCTGATGGGGGCATG
6291	Table 1	Hs.36137	AI765153	5231682	hepatocyte nuclear factor 3, gamma (HNF3G), mRNA /cds=(0,1043)	-1	CCGGGAAGCGGGGTACTGGCTGTGT TTAATCATTAAAGGTACCCTGTCCG
6292	Table 1	Hs.195175	AI802547	5368019	mRNA for CASH alpha protein /cds=(481,1923)	-1	AGCCCTTCTTCAATCTTTGTACT GATGCTTCCAACTCTTTGTACT
6293	Table 1	Hs.25648	AI803065	5368537	tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), mRNA /cds=(47,880)	-1	GGGGTAGGTTAGTAATATCCACA GACCTCCGATCCAGCAGTTGGT
6294	Table 1	NA	AI807278	5393844	wf38h03.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2357909 3', mRNA sequence	-1	CTCTACCATAAGGCACTATCAGAGAC TGCTACTGGAGTGATATTGGTT
6295	Table 1	Hs.220850	AI880607	5554656	ym91d11.r1 cDNA, 5' end /clone=IMAGE:166293 /clone_end=5'	-1	TGGGGCACTTGTAAAACCTTCACAGGC CCACGTGCTGCTGCTGAAATAAAA
6296	Table 1	Hs.23096	AI884671	5589835	602254146F1 cDNA, 5' end /clone=IMAGE:4346626 /clone_end=5'	-1	TGGCAGGATAATAAGGGCATTGTT TTGCTACTTGCATATCATTGGC
6297	Table 1	Hs.179391	AI917642	5637497	wi52d11.x1 cDNA, 3' end /clone=IMAGE:2393877 /clone_end=3'	-1	GCAGGAAAGATGGGTGGTGACTG TTTTGCTACTTTTGTGAA
6298	Table 1	Hs.180446	AI948513	5740823	importin beta subunit mRNA, complete cds /cds=(337,2967)	-1	CAGGGTATCAGATATTGTGCCCTTTG GTGCCAGGTTCAAAGTCAGTGCC
6299	Table 1	Hs.7557	AL042081	5421428	FK506-binding protein 5 (FKBP5), mRNA /cds=(153,1526)	-1	AGGCTGCATATGGATTGCCAGTCAG CATA TAGGAAATTAAAGACATTGT
6300	Table 1	Hs.39911	AL138429	6855110	mRNA for FLJ00089 protein, partial cds /cds=(62,1111)	-1	TTAAGAACCCAAAGATTAAAGGAA CAATGTTAAGGGCTTTGTGAGGA
6301	Table 1	Hs.13144	AL521097	12784590	HSPC160 protein (HSPC160), mRNA /cds=(53,514)	-1	GATAACACTGTCCAGGCCAGTCCAG GCCCTAGGTTCTTACTCTAGTAC
6302	Table 1	Hs.26670	AL540260	12870241	AL540260 cDNA /clone=CSODF032YF03-(3-prime)	-1	ACTCAGGTGGTGTGGTGTAGTGT GCTGGAGAAGAGAATATTACTGGT
6303	Table 1	Hs.183232	AL561892	12909772	hypothetical protein FLJ22638 (FLJ22638), mRNA /cds=(12,476)	-1	AAACACAGCCCACCCCATTCAGACC GCCTTCTGAGGAGAAAATGACAG
6304	Table 1	Hs.5057	AL578975	12943566	AL578975 cDNA /clone=CSODK012YN01-(3-prime)	-1	TTGGCCCAGTGTGATTGATTGCTTTA TCTTGGTACTTTACTTGAATGG
6305	Table 1	Hs.198298	AL582354	12950255	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), mRNA /cds=(297,5015)	-1	AGCCTGAGGCAAATAAAATTCCAGTA ATTCGAAGAAATGGGTGTTGCCAA
6306	Table 1	Hs.101370	AL583391	12952309	AL583391 cDNA /clone=CSODL012YA12-(3-prime)	-1	AGGACCTTGACAAGCCGTTGAGATG GAATGTTAGGCCCTGATGTTATGCT
6307	Table 1	Hs.38218	AV659358	9880372	602569368F1 cDNA, 5' end /clone=IMAGE:4693744 /clone_end=5'	-1	TGTAAGTTGACTTCAAAGTCCTG GAAACACTGGACTTTAGCTGGTCC
6308	Table 1	Hs.301704	AW002985	5849991	eomesodermin (<i>Xenopus laevis</i>) homolog (EOMES), mRNA /cds=(0,2060)	-1	AACAGCCATGTTGCCCTAGTCCAG GATTGCCCTCACTTGAGACTTGCTA
6309	Table 1	NA	AW027160	5885918	wt72008.x1 Soares_thymus_NHFTh cDNA clone IMAGE:2512983 3' similar to contains Alu repetitive eleme	-1	ACCGCCAAAGCCAATCATCCACTTTC AGTACTTACCTAACCAATCTCCCA
6310	Table 1	Hs.89433	AW071894	6026892	ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 1, mRNA /cds=(196,4791)	-1	TTTGGGGATCCTTTGTAATGACTT ACAGTGGAAATGCGAACATTGCA
6311	Table 1	Hs.335449	AW136717	6140850	Ui-H-B1-adm-a-03-0-Uis1 cDNA, 3' end /clone=IMAGE:2717092 /clone_end=3'	-1	TCTGGCCTTGTGTTACCTAGAAACGC TATTTCTGTGTTATGGTTCTGGC
6312	Table 1	Hs.12035	AW137149	6141282	602122419F1 cDNA, 5' end /clone=IMAGE:4279300 /clone_end=5'	-1	GGGTTACATTGAGTCTCTGTACCTG CTTGGAAAGAAAATAAAATACGTGT
6313	Table 1	Hs.337727	AW161820	6300853	au70h03.x1 cDNA, 3' end /clone=IMAGE:2781653 /clone_end=3'	-1	TGTGGGCTTGGTATAAACCTACTTT GTGATTGCTAAAGCACAGGATGT
6314	Table 1	Hs.81248	AW166442	6397967	CUG triplet repeat, RNA-binding protein 1 (CUGBP1), mRNA /cds=(137,1585)	-1	ACTGGCAAATGAAGCATACTGGCTTG CAGGGACCTCTGATTCAAGTACA
6315	Table 1	Hs.166975	AW293159	6699795	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(218,541)	-1	CTCCCATCATCCCTCCCGAAAGCCA TTTGTTCACTGCATCCACGC
6316	Table 1	Hs.326348	AW338115	6834741	tp39g05.x1 cDNA, 3' end /clone=IMAGE:2190200 /clone_end=3'	-1	GGCGTTCCCATGACCAAGTTGACC CTGGTTGAATAAGAGAAGTGC

Table 8

6317	Table 1	Hs.337986	AW440517	6975823	Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336,1494)	-1	GCCAGTCTCTATGTGCTTAATCCCT TGTCCCTCATTAAGCAAAACTA
6318	Table 1	Hs.250	AW444632	6986394	xanthene dehydrogenase (XDH), mRNA /cds=(81,4082)	-1	TGCAATGAGGCAGTGGGTAAGGTT AAATCCTCTAACCGCTTTGAATCA
6319	Table 2	Hs.335815	AW444812	6986574	UI-H-BI3-ajy-d-11-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2733380 /clone_end=3'	-1	TGGCAACTTCACACTCTTGATGGCGA TAATCTCTGGTATGAATATGAGCC
6320	Table 1	Hs.342873	AW451293	6992069	RC3-HT0230-130100-014-g06 cDNA	-1	TGCTTGGGAAATTGGTTGAAACC TAAAATAGCCCTTATTCGGGGA
6321	Table 1	Hs.342735	AW452096	6992953	UI-H-BI3-alo-d-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3068186 /clone_end=3'	-1	CTTCTGCCTGAAGCTGCCCATGA CTCCCTCTTGTGCAAAAGCATG
6322	Table 1	Hs.80618	AW510795	7148873	hypothetical protein (FLJ20015), mRNA /cds=(31,522)	-1	ACCCAGTTGTGCATAGTCATGATC CTCTATAAAACCACTTTGTGGA
6323	Table 1	Hs.259842	AW614193	7319379	cDNA FLJ11025 fis, clone PLACE1003968, moderately similar to 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT /cds=(159,1145)	-1	ACACCATTTCAGCGTGGATCACAGA CAGCTCTCCCTTATATCCAGCA
6324	Table 1	Hs.334437	AW778778	7793371	hypothetical protein MGC4248 (MGC4248), mRNA /cds=(70,720)	-1	TGGCATAATGTTGGATTGAATCTACA TTTGGCAGAAGTTAACATTCCC
6325	Table 1	Hs.151393	AW778854	7793457	glutamate-cysteine ligase, catalytic subunit (GCLC), mRNA /cds=(92,2005)	-1	AGAATGCCCTGGTTTCGTTGCAATT TGCTTGTGAAATCAGGTTGAAA
6326	Table 1	Hs.120243	BE044364	8361417	gamma-parvin (PARVG), mRNA /cds=(0,995)	-1	ATCGTTGGATTATCTTGAACCCCCCT TGTGTGGATCATTGAGCCGCC
6327	Table 1	Hs.5734	BE218938	8906256	meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(395,3145)	-1	ATACAGGGTTCATCCAGAAAGCATT CAGTCAGAGCAAGTTAAAGTCAGT
6328	Table 1	Hs.167988	BE222301	8909619	neural cell adhesion molecule 1 (NCAM1), mRNA /cds=(201,2747)	-1	AAGTTGCTCTGTGCTAAAGCAAGCGT GGGATGATCCTACCTACCTCTAGG
6329	Table 1	Hs.27774	BE348809	9260662	602386841F1 cDNA, 5' end /clone=IMAGE:4515730 /clone_end=5'	-1	AGCTAGTGTGTTGTCCAAGGAA GATTCTGACAACAGCTTCAGCAGA
6330	Table 1	NA	BE348955	9260808	hs91h01.x1 NCI_CGAP_Kid13 cDNA clone IMAGE:3144625 3', mRNA sequence	-1	ACACAGACATATTGACCGCACACAAC ACTGAAATGGACTGACTTGAGAAA
6331	Table 1	Hs.56156	BE349148	9261087	601463367F1 cDNA, 5' end /clone=IMAGE:3866512 /clone_end=5'	-1	TGGTTCTGTGATTGTAATGAGCACC TGGATATGTCATAAATGCCCA
6332	Table 1	Hs.127428	BE466500	9512198	Homo sapiens, Similar to homeo box A9, clone MGC:19648 IMAGE:2987818, mRNA, complete cds /cds=(62,880)	-1	GGCCTACTGACCAAATTGTTGTTG AGATGATATTTAACCTTTGCCAA
6333	Table 1	Hs.122575	BE502246	9704654	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4 (EDG4), mRNA /cds=(6,1061)	-1	CGATAGAATTGAAGCAGTCCACGGG GAGGGATGATAAGGAGTAAC
6334	Table 1	Hs.197766	BE502992	9705400	clone 23932 mRNA sequence /cds=UNKNOWN	-1	CTCAAACGAAATTGGCAGGCCATT GCGTGGTTCTGGATAAGTTCC
6335	Table 1	Hs.61426	BE550944	9792636	602329933F1 cDNA, 5' end /clone=IMAGE:4431248 /clone_end=5'	-1	GCACATGACAGTAAGCAGGTTTGG GTAAATATAGATGAGGATGCCTAT
6336	Table 1	Hs.122655	BE551867	9793559	hypothetical protein MGC14425 (MGC14425), mRNA /cds=(318,686)	-1	ACACAGGAACCGCTTACCCACAGCT CTGCCCGCGTCTCACGCCATAG
6337	Table 1	Hs.4310	BE614297	9895894	eukaryotic translation initiation factor 1A (EIF1A), mRNA /cds=(207,641)	-1	ACAACTCAAGTAAAAGATGTCCTCA GTTCTGAAGATAACCCACGCTGA
6338	Table 1	Hs.341573	BE646470	9970781	tc38c11.x1 cDNA, 3' end /clone=IMAGE:2066900 /clone_end=3'	-1	AAAACACTCCACCTAAAGCAGGAAA GATGCGAATTCTAAATAGCAGCTA
6339	Table 1	Hs.88845	BE674685	10035307	AV733781 cDNA, 5' end /clone=cDAASF08 /clone_end=5'	-1	CGCCGCTCTGGAGACCTGATAACTT AGGCTGAAATAATTGACTTGT
6340	Table 1	Hs.181015	BE676054	10036595	signal transducer and activator of transcription 6, interleukin-4 induced (STAT6), mRNA /cds=(165,2708)	-1	ATCCCATTCTCCCTCTCAAGGCAGGG GTCATAGATCCTAAAGCCATAAAAT
6341	Table 1	Hs.108327	BF001438	10701713	damage-specific DNA binding protein 1 (127kD) (DDB1), mRNA /cds=(109,3531)	-1	ACAGCATGAGAAAATGTTAGTACGCA TACCTCAGTTCAACCTTGTGGA
6342	Table 1	NA	BF056055	10809951	7k07h12.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3443950 3' similar to contains element L1 repetitive elemen	-1	CACAATGCTGCCCTCTGTGGATGA CTGATGCCAGAGTCTGAATTGAA
6343	Table 1	Hs.43857	BF058599	10812495	mRNA for KIAA1247 protein, partial cds /cds=(285,2942)	-1	TAAGAAATCCCAATTTCAGGAGTGG TGGTGTCATAAAACGCTCTGTGGC
6344	Table 1	Hs.144583	BF059133	10813029	Homo sapiens, clone IMAGE:3462401, mRNA, partial cds /cds=(0,153)	-1	CGGCAGGGTGGCCTGTAACAATTTC GTTTCGCGAACATTCAAGGTATT
6345	Table 1	Hs.144519	BF061421	10820331	T-cell leukemia/lymphoma 6 (TCL6), transcript variant TCL6a2, mRNA /cds=(1767,2192)	-1	GCTGGAGGGAGAGGCACTGGGAAT TTTCCTGGTGAATCTGAAGTTAC

Table 8

6346	Table 1	Hs.96566	BF194880	11081165	602137338F1 cDNA, 5' end /clone=IMAGE:4274048 /clone_end=5'	-1	TGATACTTGGTCTCTTCCTGCTCA GGTCCCTTCATTGTACTTTGGA
6347	Table 1	Hs.111583	BF197608	11086855	602365742F1 cDNA, 5' end /clone=IMAGE:4473923 /clone_end=5'	-1	ACTGCCAGTGAAGACTGTAAAGACAG AACACACTATTTGGAGGGAGGAT
6348	Table 2	NA	BF197762	11087169	7p11f02.x1 NCI_CGAP_Skn1 cDNA clone IMAGE:3653139 3', mRNA sequence	-1	AGGAAGAGCCTGCACCTGTGGTGA ACAATCAGGGAAAAGGAAGTCAAA
6349	Table 2	Hs.50785	BF221780	11128957	SEC22, vesicle trafficking protein (S. cerevisiae)-like 1 (SEC22L1), mRNA /cds=(119,766)	-1	TTGGAGCTTCTATAGGAGTGGAGAG GGGCAGCTCATTTGAGAGTTGC
6350	Table 1	Hs.250811	BF432643	11444808	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB), mRNA /cds=(170,790)	-1	TGATCTGACTGGAAAACATCCTGTA TCCCCTCCCAAAGAATCATGGGCT
6351	Table 1	Hs.293476	BF435621	11447923	hypothetical protein FKSG44 (FKSG44), mRNA /cds=(126,1520)	-1	CGTTTCTGAGCATCCGTTGCGCTT AACATTTCTGCTTGCTTTGGG
6352	Table 1	Hs.174104	BF445405	11510543	601438710F1 cDNA, 5' end /clone=IMAGE:3923643 /clone_end=5'	-1	ACTGTGTTGCATGAATAGATGATAC AAAGCAAGTGTAGGTTGGTAG
6353	Table 1	Hs.295726	BF447885	11513023	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) (ITGAV), mRNA /cds=(41,3187)	-1	AGTAAAAACTGGTACAGTGTCTGCT TGATTACACATGTAACTTGTGA
6354	Table 1	Hs.181311	BF478238	11549065	asparaginyl-tRNA synthetase (NARS), mRNA /cds=(73,1719)	-1	TGTCCTCTGAACCTGAGTGAAGAAAT ATACTCTGCTTGTACCTGCGT
6355	Table 1	Hs.179703	BF507849	11591147	tripartite motif protein 14 (TRIM14), mRNA /cds=(10,1230)	-1	CCATTCTCACTACATGCCTTCTAC CTTCCTTCAACACCAATCAAGTG
6356	Table 1	Hs.300870	BF513802	11598781	mRNA; cDNA DKFZp547M072 (from clone DKFZp547M072) /cds=UNKNOWN	-1	AATACAGATTCACTTTATTAAAGCGTC CGTGGCACCGACAGGACCCAG
6357	Table 1	Hs.283022	BF514341	11599520	triggering receptor expressed on myeloid cells 1 (TREM1), mRNA /cds=(47,751)	-1	GCTCTTTCCGTATCACACAAGGG TCAGGGATGGGGAGTAAAAGCTC
6358	Table 1	Hs.146065	BF591040	11683364	AL580165 cDNA /clone=CSODJ005YB18-(3-prime)	-1	CTGGGGCCGTAGCAAAATCATGAA AACACTTCAACGTGTCCCTTCAAT
6359	Table 1	Hs.170577	BF725383	12041294	602574255F1 cDNA, 5' end /clone=IMAGE:4702644 /clone_end=5'	-1	CAGACCTGTGGGCTATTCCAGACT GAGAGTTGAAGTTGTGTGCATCA
6360	Table 1	Hs.104640	BF726114	12042025	HIV-1 inducer of short transcripts binding protein (FBI1), mRNA /cds=(0,1754)	-1	AAGGCAACCAACCACATTAGAAGTCT TGGCACTTGTAAACGGAACGGGTA
6361	Table 1	Hs.296317	BF938959	12356279	mRNA for KIAA1789 protein, partial cds /cds=(3466,4899)	-1	GAAGTGACACTGACTGTATCTACCTC TCCTTTCTTCATCAGGTGTTCCCT
6362	Table 1	Hs.26136	BF940103	12357423	hypothetical protein MGC14156 (MGC14156), mRNA /cds=(82,426)	-1	AATTCCAAAGGAGTGTAGTGGAAATA GTCCCTCTAAAGGGAGAGAAATGCA
6363	Table 1	Hs.133372	BF940291	12357611	AF150127 cDNA /clone=CBCBGA01	-1	AGCCCCCTCCACCCACCCAGTACTTT TACAATGTGTATTAAAGACCCCT
6364	Table 1	Hs.304900	BF980139	12347354	602288147F1 cDNA, 5' end /clone=IMAGE:4373983 /clone_end=5'	-1	CCATCCTTGAGAAATGTGGGACCAA GTCCATAATCTCCATAAAATCCAAT
6365	Table 1	Hs.8258	BG054966	12512220	cDNA FLJ14737 fis, clone NT2RP3002273, weakly similar to SCD6 PROTEIN /cds=(77,1468)	-1	TATGAGTTATGCGTTTCCAGCCC TCCGAATCACTGACTGGGGCGTT
6366	Table 1	Hs.5122	BG058599	12525258	602293015F1 cDNA, 5' end /clone=IMAGE:4387778 /clone_end=5'	-1	AGTTGGAGCTATCTGTGCAGCAGTTT CTCTACAGTTGTGCATAATGTTT
6367	Table 2	Hs.89104	BG058739	12525527	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	CGTGGGAGGATGACAAAGAACATG AGTCACCCCTGCTGGATAAACTTGA
6368	Table 1	Hs.166982	BG149747	12661777	phosphatidylinositol glycan, class F (PIGF), mRNA /cds=(67,726)	-1	GTGGTTGGTCAGCATACACACTCT CATTTCATTGTGTACACAGCCA
6369	Table 1	Hs.184456	BG230563	12725586	hypothetical protein (LOC51249), mRNA /cds=(0,611)	-1	GTGTGAAGTGCACGCCCTGTGTGA TTGTTTCTGCCTTCCCAAGTTTG
6370	Table 1	Hs.3353	BG236015	12749862	beta-1,3-glucuronidyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA /cds=(175,1179)	-1	GTCTTCCCGTCTTCTTCCACCTA TGTAATTCAGTAGTCTCTCAGC
6371	Table 1	Hs.83623	BG654774	13792183	nuclear receptor subfamily 1, group I, member 3 (NR1I3), mRNA /cds=(272,1318)	-1	TGTTTCGTAATTAAGGTCTGGC CCAGAAGACCCACTCAATTGCCCT
6372	Table 1	Hs.109007	BG655723	13793132	602342214F1 cDNA, 5' end /clone=IMAGE:4452602 /clone_end=5'	-1	GTGGAATTCAGCACACAACCAATG ACATTAAAGCACAGGATCATTATT
6373	Table 1	Hs.14453	BG744911	14055564	interferon consensus sequence binding protein 1 (ICSBP1), mRNA /cds=(47,1327)	-1	AGAATGGCAGACCTGTTGCTGAAGT GTTCATAAGATAACAATAGGCTTG
6374	Table 1	Hs.2730	BI084548	14502878	heterogeneous nuclear ribonucleoprotein L (HNRPL), mRNA /cds=(28,1704)	-1	TGGGATTTGTTTTAAAGTCATTGGT TTGGGGAGGACCTTGTGTTATTTT
6375	Table 1	Hs.298356	BI085832	14504162	mRNA; cDNA DKFZp434M162 (from clone DKFZp434M162) /cds=UNKNOWN	-1	TGGACAAACTGACAGGGACTGCTTG AAAGACAGGTACTCAGTTGAGTAT

Table 8

6376	Table 1	Hs.132911	N20190	1125145	MR2-OT0079-280500-007-b03 cDNA	-1	AAGCCTGTTTCACTCTAAAAATTCA AGAGGACACCTAAGAACGATCA
6377	Table 1	Hs.334731	N58136	1202026	Homo sapiens, clone IMAGE:3448306, mRNA, partial cds /cds=(0,2353)	-1	AGGTTCCTTCAAATAAGATAAAG AATTGACTTGGACACTGCCAGA
6378	Table 1	Hs.303018	N94511	1266820	zb80g04.s1 cDNA, 3' end /clone=IMAGE:309942/clone_end=3'	-1	CTGTTCGAAAGTTGGAGACTGCCTGT ACCCAGGTGATACTCAATTGTTT
6379	Table 1	NA	W68708	1377588	zd35h04.s1 Soares_fetal_heart_NbHH19W cDNA clone IMAGE:342679 3', mRNA sequence	-1	AGCAGAGTTAAGTTAAATTCCATT TCACTAGTTGACCTTGCCA
6380	Table 1	NA	W86427	1400194	zh61c11.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:416564 3', mRNA sequence	-1	TGAGTATTGTTGGGGGGGGTAT GTCTGTATATAATCTGTGCAGCCA
6381	Table 3A	NA		36G5		1	CCCTTGCAGATACATGAGACAGGCA GGGCTGGAGTCTTGTCCATCTG
6382	Table 3A	NA		36F11		1	GAGTAGTTGCTTCTGTGCACTAAC GTTGAGCTCGTGTACGCAGTAAG
6383	Table 1	NA		37G7		1	GAGTCCAATCTACACTCTAGTAGTGA AGACAGAAAGAGTTGGCATACGAAT
6384	Table 1	NA		37G8		1	GGCTGAACTTACTCATTAAGCCACAT AACTCGAGTCAGTTCCAGTC
6385	Table 3A	Hs.197345			thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA /cds=(17,1848)	1	GCTCTAACGCTCTCCAATAAGCT CTATCGGGAAACAAATGAACAGT
6386	Table 1	NA		40E4		1	AGGAATGCACACATTGCTCCAGGATC ACTGTGAGGATTAAGGAGATGGT
6387	Table 3A	NA		41E9		1	AGTAACGGAACAGTCCCCAGTACTCC TGGTCTCCTAGGTGAGCAGGTGATG
6388	Table 3A	Hs.169476			Homo sapiens, glyceraldehyde-3-phosphate dehydrogenase, clone MGC:10926 IMAGE:3628129, mRNA, complete cds /cds=(2306,3313)	1	GGTGTGAACCATTGAGAAGTTGACAA CAGCCTCAAGATCATCAGCAATGA
6389	Table 3A	NA		47E5		1	GGAGGTGTATAGGCTGGATTGAAA AGGAAAATAATCAGCGTGGTCCA
6390	Table 2	NA		47D11		1	CCTAGACACCTGCATCAGTCAGGTC ATGATATTGGGAAAGACAGACAGC
6391	Table 1	NA		50A11		1	TCCAGCAGATATAGAAGCAGTGTAT CTAAACAGACAAATAAAAGGCT
6392	Table 3A	Hs.132906			DNA sequence from clone RP11-404F10 on chromosome 1q23.1-24.1. Contains the 5' end of the SLAM gene for signaling lymphocytic activation molecule, a SET (SET translocation (myeloid leukemia-associated)) protein pseudogene, the CD48 gene for CD48 antigen (B-cell membrane protein), the gene for a novel LY9 (lymphocyte antigen 9) like protein and the 5' end of the LY9 gene. Contains ESTs, STSs and GSSs /cds=(41,1048)	1	ATCTAGTGTACGAGACTTGGAGTCAG GCAGTGAAGACTGGGGCACGGG
6393	Table 1	NA		52B9		1	TGGTTTAATGGAAAATGCTCTGGAAA ATTCTTTGCAACAGTCATCGCT
6394	Table 1	NA		53B1		1	CACTAAAAGAGTGGGGAGGTGCAGC ACCTGGCTGGGGAAACAAGAATATGG
6395	Table 1	NA		53E3		1	AAACGAATCACGTGCCTCGAAAGGG ACATATAATTGTTCTTAAAGCATT
6396	Table 1	NA		53E10		1	AAGGGTTCAATTCTCTTGGAAAGG TGATGGTAAGGGTGTGCTCCAGA
6397	Table 2	NA		53G7		1	TGGACAATTCCAAGTCCAAGAGGACT GTCTACTTTCGACCTTGTGTGATT
6398	Table 1	NA		54F4		1	TTGTGTTAACCTGTTGTCCACGCTAA GATACAAAATTCCCGAGGAAAGT
6399	Table 1	NA		54G9		1	TGTCACAGTGTCTATTATTGCCCCG GTTCTAAAGTGAGAGCATCTGA
6400	Table 1	NA		59G1		1	ACAAATGATATTGATGAGGCACCCAGT CTTTTCAATTACTCTGAGTGAAGT
6401	Table 1	Hs.48320			mRNA for ring-IBR-ring domain containing protein Dorfin, complete cds /cds=(317,2833)	1	AGATCGAGATCTTCAGTCCCTCTGCTT CATCTGTGAGCTTGCCTTCAGTC
6402	Table 1	NA		60G8		1	GGCCAGAGACCTAAGCTGCTTAATA CATTATACACATCCTCTCAGC
6403	Table 2	NA		62C9		1	CCCTTGGATTACTGTGCAACTCTT TCTTTCGCACTAGACGGGGACTT
6404	Table 3A	NA		62F11		1	CTTTGTAGATGCAGAGAGAAGCTATA AGAAACCCCGAGTACTTGGCGGGCG
6405	Table 1	NA		63E1		1	ACTGCCACATCTGACTTTACAGAATA ACCAATGTAAGTTAAATAGAGAAC

Table 8

6406	Table 2	NA	65B1	1	AGTCTTGCGAGTCAACTCAGACTCAA ATGTAGAACGGAGGACAGTC
6407	Table 2	NA	65D10	1	AGCACTGTGCAGATGGCTTTAGAAGA TTCAGAACAGAACACAATCTGTT
6408	Table 2	NA	65D11	1	AGCACTGTGCAGATGGCTTTGGAGA TTCAGAACAGAACACAATCTGTT
6409	Table 2	NA	65D12	1	CTATGGAGTCTGGAGGACACTGGA GTCAACCAGTCTAACACTGTGCAGAT
6410	Table 1	NA	68C9	1	CCCTGTCACCCCTCGTGGCCAGTGC CAGACAGTAACTAGTGGATGCTAA
6411	Table 1	NA	69F8	1	GAGAGAATAGGGTAGAGAGACCGGG ACTTGGGTAGAGATGACCGGGATTG
6412	Table 1	NA	69H11	1	AGTGGAAAGCTAGGAGAAAATATCGAAT GTGTTAGGGACTTTAGGTTACCA
6413	Table 3A	NA	70B8	1	CTGCATCTCTCTTACTACCACTGATT ACAAAGTGGGGTTGGTGGGAGT
6414	Table 3A	Hs.17109	integral membrane protein 2A (ITM2A), mRNA /cds=(139,930)	1	TCTCTGACTTCTTATTACCAAGGACA CTCTATCTGTTGCCCTTACTCTT
6415	Table 2	NA	72D4	1	CAGTTCCCAGATGTGCGTGTGTTGGT CCCCAAGTATCACCTTCCAATTT
6416	Table 3A	Hs.234279	microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA /cds=(64,870)	1	AACGACCCCTGATTGAGAAGATTG AGACATTCTGTATGCCACAGATGA
6417	Table 2	NA	72D8	1	GGGTCGGAGCCCTCAAGAGCTAG ATTACTCAAGTTGTTCCCTTGCC
6418	Table 1	NA	73C4	1	CACTGAAGCCAACACACAGAACAGCTT TTGAGAATGAGGAGACAAATGAGT
6419	Table 1	NA	73H4	1	AGGTGAAAATTACTCTTCAGAAAGATA GCAGAGTGGATAATGGCCCATCGA
6420	Table 2	NA	73A7	1	TGCAGTGTGAGTACATTTCTGCTAA AGAAGATGTGAGTCCGTCCCTT
6421	Table 3A	Hs.174228	small inducible cytokine subfamily C, member 2 (SCYC2), mRNA /cds=(0,344)	1	TCCAGCCAGCCAGCTCATTTCACTTT ACACCCCTCATGGACTGGGATTATA
6422	Table 3A	Hs.3945		1	TTTCATACATTGGAACCTCCACCTGAC TTTGGACCAACCCAGAACAGAGC
6423	Table 1	NA	75A2	1	AGCACCGGAATACAAAATGATACTA TGCTGCCCTCCTAGATCTCAGGGA
6424	Table 3A	Hs.249495	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA /cds=(104,1222)	1	TGCCCATACACATGAGTATTGTCTAA AAACATGTCTTCTTGAGCAGCT
6425	Table 2	NA	75B12	1	GCAAATCTAAACTGCAGGAAAATTT TGACCCCGAAGTATTAGATCCCT
6426	Table 2	Hs.205442	601439689F1 cDNA, 5' end /clone=IMAGE:3924407 /clone_end=5'	1	GGCCCACTGCTAATGTAACCAATGAT GCCATGTCGATATTGAAACCCATA
6427	Table 3A	NA	101G7	1	GGGGAAAGAACAGATAATCTAGTGC CTCACCACTGCTATGCCAGGGC
6428	Table 3A	Hs.179565	minichromosome maintenance deficient (<i>S. cerevisiae</i>) 3 (MCM3), mRNA /cds=(44,2470)	1	AATTCAACTGAAAGGAGCTAGTGG GTGATGAAGCTGAGATCAGGACTC
6429	Table 1	Hs.119640		1	CACCTATATCGAAAGTTGGCTCAT CTCCCCATTGGTGGCAAAGACCTCC
6430	Table 3A	Hs.215595	hBKL for basic kruppel like factor (LOC51274), mRNA /cds=(55,1092) guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA /cds=(280,1302)	1	TGGTGGAAAAGTGTCTGTCTGACA ATTACACTCAAGTTACCTCTGTT
6431	Table 1	NA	105A10	1	ACGATAATACTGTTGTTACTGCCAT AAATATTGGAAGCTAATGAAAATGC
6432	Table 1	NA	107G11	1	TTCTCTTATAAAGGACAGCAAGTTAA AATGGAGCAAGGAGCATTGAAA
6433	Table 1	NA	107H8	1	TGGCAAAGAAATAGAAGCTCTAGACC TTCCCTATTCTATCGTGAACAA
6434	Table 3A	Hs.64239	DNA sequence from clone RP5- 1174N9 on chromosome 1p34.1-35.3. Contains the gene for a novel protein with IBR domain, a (pseudo?) gene for a novel protein similar to MT1E (metallothionein 1E (functional)), ESTs, STSs, GSSs and two putative CpG islands /cds=(0,2195)	1	ACATGACCTGTGCACTGTGTGGCTGT GAATTCTGTTGGCTTGTATGAAA
6435	Table 1	NA	109H9	1	TGACATAACTACCATCCCTGCAACTA ATGAACCCACCCCTCACAGCTTCCT
6436	Table 3A	Hs.80261	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related) (HEF1), mRNA /cds=(163,2687)	1	GAATGACATAACCCCTCCGGTCTG AGGTCCGGCTTCCAGCTTGTCTC
6437	Table 3A	Hs.1422		1	GCCTTCTCACTCCATCCCCACCCAA AGTGCTCAGACCTTGTCTAGTTAT

Table 8

6438	Table 3A	Hs.333114	AV713318 cDNA, 5' end /clone=DCAAAC09 /clone_end=5' 129A12	1	TCGTTTACAACGTGCGTACTGGAA AACCCCTGGCGTACCCAACCTAAAT
6439	Table 1	NA	129F10	1	TGTTTGTTCTGAAACGAAATCCTG CTCTGTTGGCCAGCTAGAACGC
6440	Table 1	NA	137D4	1	CAGAAGCTGGATGACGTTGCTCATC TTCACTCTTTAATGAGACATGAT
6441	Table 3A	NA	142F9	1	CACATCTCCATTAGCCCTACCATG AAAACCGTACCTCGGGCGGCCACCA
6442	Table 1	NA	prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(155,487) heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA /cds=(104,1222)	1	AATTGCTTTAAATTGAGTTTCTTGC CATTGCACACTCTATCTTCTG
6443	Table 3A	Hs.250655		1	CAGATGACACCGCGCTCTCCACCACC CAACCCAAACCATGAGAATTGCAA
6444	Table 3A	Hs.249495		1	CCCATGCTGTTGATTGCTAAATGTA CAGTCTGATCGTACGCTGAATAA
6445	Table 1	NA	149G2	1	GACACAGACAGACCAAGCTATAGTC GACCTGGTTACACACATACACACA
6446	Table 1	NA	149A11	1	TGGAAAGATCACTGAATTAGGAC ACCAAAGCTAAACCCCAATGCT
6447	Table 3A	NA	151F11	1	GCTTGTGCTCGAGACCGCTGGCTATA GAAACGCTGAGCTGCTGGTTATG
6448	Table 1	NA	162E8	1	CTGGTTAAAGCCCCATTACTGACCT TCGCCGCCACACGCCCTACACTA
6449	Table 3A	Hs.334330	calmodulin 3 (phosphorylase kinase, delta) (CALM3), mRNA /cds=(123,581)	1	GCATCCACCTCCTCTGTCTCATG TGTGCTCTCTCTTACAGTA
6450	Table 1	NA	170F7	1	TTAAATCTATCAAGAATTATCCTAAAT TGGTACCCCTGCCGGGCCCTCG
6451	Table 2	NA	170F9	1	AGTGTGTTATTGACTTTGCTCGGCAG TAGATGAAGCTATTCTGAACCCAA
6452	Table 3A	NA	177A3	1	TGCTGGACAAAGACAATGAGATGATT ATTGGTGGTGGATGGCTGTTTAC
6453	Table 1	NA	331A3	1	GTGGAAGATCACTACCAAGGGCTGGC AGGGAAATGGGCAATCTATTCTAC
6454	Table 1	NA	331A5	1	AAGGGACAGGGAGCGGGCACAAAAT AAAACCTAGTTGGTAGAAATTATA
6455	Table 3A	NA	146C3	1	TCAAAGCACTGGAGATGAGAGCCAG GATGGACCCAAAAAGAATTACAG
6456	Table 1	NA	146D8	1	CAGGAACATGGCTGCAGCATATAAAA AGAATTGAATTCCATACCTTTGTTAAC CCT
6457	Table 3A	Hs.153	ribosomal protein L7 (RPL7), mRNA /cds=(10,756)	1	TTGCCATAACACACGCTTGTAGATTAG TTCATTACTGACTTCAGATTGGG
6458	Table 1	NA	158G6	1	TTACAGGCAACCGGAGCATCCAATCA CCTTCTCTAAAGAGAGTACCTCGG
6459	Table 1	NA	158H6	1	AAAAGCATCTCGAGAGGGACTGTCA ATTCTGACTATTCTCAACCCGC
6460	Table 3A	Hs.119598	ribosomal protein L3 (RPL3), mRNA /cds=(6,1217)	1	AAGAAGGAGCTTAAATGCCAGGAACA GATTTCAGTTGGTGGGTCTCAA
6461	Table 1	NA	158E9	1	AGAGACACCTAAATTACAGATTGTG AGCTGAGAGCTGGAGTTTTCTATT
6462	Table 3A	Hs.326249	ribosomal protein L22 (RPL22), mRNA /cds=(51,437)	1	AACAGCAAAGAGAGTACGAATTACG TTACTTCCAGATTAACCAGGACGA
6463	Table 3A	Hs.297753	vimentin (VIM), mRNA /cds=(122,1522)	1	AGCGCAAGATAATTGGAAATAGAA TAAGCTCTAGTTCTAAACACCGA
6464	Table 3A	NA	155H10	1	GCATGGACAAGATGCCAAGGCCGG ATGCTTTAGGATGAAAGTTCTTATCT
6465	Table 3A	Hs.108124	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	1	CCTCCAGTCACCATACACAGGTTACCC AGTGTGAACTTGTGAAATCACT
6466	Table 1	NA	159F6	1	CCAAACATCTGGACTTGTGACTGTAA AAGGGGAGGAGGTAACCAATGATT
6467	Table 3A	NA	166F3	1	TTATGGTGGTGGGGTGGGTGGTAG TTCAATGGGAGGTATGGGATTATT
6468	Table 1	NA	166F6	1	AGCTGTCTGGCTCAAAGATCTACATT CTGAATTGGCTGGAAATGTCTTG
6469	Table 1	Hs.8121	Notch (Drosophila) homolog 2 (NOTCH2), mRNA /cds=(12,7427)	1	CTGGTTCTACCAAGTGCCAGTGCCT CAGGGCTTCACAGGCCAGTACCTC
6470	Table 2	Hs.25130	cDNA FLJ14923 fis, clone PLACE1008244, weakly similar to VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1 /cds=UNKNOWN	1	TGACACAGACTTTCAATCTGGAG CAGCGACTGACTTTGACAGAAGAT
6471	Table 1	NA	168A9	1	TGCTTTAAAGCACCAGTATAATAT GAGGCCACTTGGAAATCCATCCA
6472	Table 1	NA	171F11	1	GCAGGGCGATGCTCTATAATCTAAAT GTATCTCTCTTCCCTAAAGCTGAA
6473	Table 3A	NA	171G11	1	AAGTAAGACCACCTGTGAACCTGATC ATTATCTGGCGCACATAGGAAGAT
6474	Table 1	NA	175D1	1	GCTGGGGCTGGGAATTGCGTGGGCT AATGTTGTCATTGACTTAAGAAACT
6475	Table 1	NA	182H1	1	TTTGGGAAGAACCGATTGCTAAATTA TGCCTAATTGTCAGAAGAGGG

Table 8

6476	Table 3A	NA	184B5	1	AAGCAGTATAACCATTATAGCAAA CAGCCAGTGGCCAGTCACTGTAT
6477	Table 3A	NA	184D2	1	CTGCCCTTGGTAGTGAGAGGACCA CGCCAATGATGCTTTAAAGTAACCT
6478	Table 1	NA	184H1	1	CATTCTTCATCTAAGGCACACTT GCTACCCCTTTGCTGACCCCAG
6479	Table 1	NA	46D1	1	GCCTGCCTGCTGTCTCAGTGTTC TGTCCTCCTCTAAGTACTCTAAA
6480	Table 1	NA	98C1	1	AATCCTAGACATGTGCTTGTCTTG TCCCATGAAGGTAGTTCAAAACA
6481	Table 1	NA	98C3	1	ACCAATAGAGAAGAAGCTCTAGAAGA CAAATCCCAACCTTGGCACAAA
6482	Table 2	Hs.205442	601439689F1 cDNA, 5' end /clone=IMAGE:3924407 /clone_end=5'	1	GGCTTCAACAGAAACATCAAATGCCA AGACCAAGTGAAGAGAGCGTCAAAAAA
6483	Table 1	NA	98H4	1	GCAAGCCCCTAAATAAACATCTAA CCAGCATTTCCCCATTATAGG
6484	Table 1	Hs.169363	GLE1 (yeast homolog)-like, RNA export mediator (GLE1L), mRNA /cds=(87,2066)	1	ATGGATCTTCTCTGTGCTAAATG TCTTGTGGCAGGGTGTGTTGTGG
6485	Table 3A	NA	113F12	1	GCCGTAATGTCTCGGGATCTCTAATA ATAGAGGAGGTGAGTTGTGGTGTC
6486	Table 1	Hs.30212	thyroid receptor interacting protein 15 (TRIP15), mRNA /cds=(15,1346)	1	AGGCACTCCTCAACCAGTGTTCACTG AATTCAACTGCTGAAATTGTAACA
6487	Table 3A	NA	173A10	1	AGAGAGGGTTTAAAGGGAGGCCCTG TGAATACTGGGAGAATACGGAAGG
6488	Table 3A	Hs.334853	hypothetical protein FLJ23544 (FLJ23544), mRNA /cds=(125,517)	1	ATGAATTGAAGACATGGTGGCTGAA AAGCGGCTCATCCCAGATGGCTGT
6489	Table 3A	Hs.20252	DNA sequence from clone RP4- 646B12 on chromosome 1q42.11-42.3. Contains an FTH1 (ferritin, heavy polypeptide 1) (FTHL6) pseudogene, the gene for a novel Ras family protein, ESTs, STSs, GSSs and a putative CpG island /cds=(0,776)	1	TTCCACAGATAGGTAAGCCAGGC GGCAAGATGAGACTGTATTCAAGTTA
6490	Table 1	NA	174D1	1	TCTTGTCTTAGTCATTGTGGCAACCC CATCTGACACCTTGTGAGTACCT
6491	Table 1	NA	45B9	1	TTCTGGCAAGCTTGTCTGATGGTGT CGACACTCTCTGCTCTTCTGG
6492	Table 1	NA	45H8	1	TTTCAACATGGCTAGATCCATAGAA ACTGAAGGGGGGGAGAAAGCTCT
6493	Table 1	NA	111H6	1	GGTACTCAAAGGAATTACTCTTCT CTGGAACCCCTGGCAGAAAGTTTA
6494	Table 1	NA	111E12	1	ATCCTTCCTACCTTTATTATGAAAGT TTTGTACCTGGCCCGGGGAGCG
6495	Table 1	NA	111H11	1	ATTAAGGTTTAAACATCTACTTGGG TGATGAGCCTCAATGAAGTCA
6496	Table 1	NA	112H3	1	GAAAGACTACGAATTGCTGGGAG GTAATAGGGAACCTCCACATAAA
6497	Table 1	NA	112E9	1	AAATGAGGTCAAGCAATAACCTTGT CGGTCCCTCACTGGCAACATTAA
6498	Table 1	NA	114G3	1	CTTCTCTCCCTGTAACCAGGCAGTGT GTGGGGCGGGGCTCAGAACATATCT
6499	Table 1	NA	117H6	1	GTCCCCCTGATCTGAAATCCCTGTG CTTCTCTGGGATGAAGGAACCTC
6500	Table 1	NA	165E7	1	TAAGATAACCCACAGGCACTTCTGT CATAAAGCCAACGACACAGACAG
6501	Table 1	NA	165E11	1	ATGGGAACAGGATGTTAAATACACAC ATACATACGACACAAGCGTTGGG
6502	Table 1	NA	165F7	1	CCTCTGCTACACTAGAGAATGTAGA GAATGAAATGGCTGCCCTTATGC
6503	Table 1	NA	176A6	1	GATACAGATGTGATTATTCAAGCCTCA AGGGGACTTCTCATTGCGTAACG
6504	Table 1	NA	176G2	1	TTATTGTTACCAATTAGAATCAGCAAT TCACACTGTGCGGTGATTGGCCT
6505	Table 1	NA	176E10	1	TCATCACTTGGGTTAACTAAAGGTT GCGTATCACACAACTACACTACAA
6506	Table 3A	NA	176F11	1	TTICATAGTCACACAAAGGTAAAGTC ATGCATATACCCACGGCAACAGG
6507	Table 1	Hs.232400	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(169,1230)	1	CCCACCCCTCCCTCCCATGTGAAG ATTGGGTGCTAACATATCATT
6508	Table 1	NA	71F2	1	GGGAGACATGCTGATTCCACTCAAAG ATCTCATATAAACAGCTTGGCC
6509	Table 1	Hs.172028	a disintegrin and metalloproteinase domain 10 (ADAM10), mRNA /cds=(469,2715)	1	AAATAATTGGAATGGGACATTGTG CTGTTTACCTCAATGCTTTAA

Table 8

6510	Table 1	Hs.180610	splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated) (SFPQ), mRNA /cds=(85,2208)	1	AGAACAGTCTGGGTTCAAGGGGTGT GATGCCAGAATGTATTCGTAACCT
6511	Table 1	NA	124G4	1	AAGGCGAAGTCAATCCCATCTCCCTG AACCCAATGCCAGTAGGTAGTTC
6512	Table 1	NA	124C8	1	AGTAAACTGTTGGTAGGTAGTGTG TCAGGACTCTGTATATTAGCTCT
6513	Table 1	NA	124F9	1	ACTGGATAAACAGAACGGATCAAAGA TAAAAGTATTCTTGTGCGCTGGGC
6514	Table 3A	NA	127A12	1	GTCCCCTAGGGAGGGAGGTGTC CTCTTGCCCCACAGTCTACCCCTCAG
6515	Table 1	Hs.50180	601652275F1 cDNA, 5' end /clone=IMAGE:3935610 /clone_end=5'	1	ACTGGACTACTGAACTTAGAATACT GTCCTAAGGAAATAGGTCTGGCAG
6516	Table 1	NA	161E8	1	CAAACAACAAAAGTGGCCTCCATCGC TGTGAGCCTCTCAAGGGACAGGGC
6517	Table 1	NA	186E8	1	AAGGTGGCTGGCTTTTATGATAACAGT GGTGGTAATGTAGCCCTTTGGT
6518	Table 2	NA	191F6	1	TGCTCAATTGCCATACATGCACTATA GGCCGGGATAGAAAATCGTCAGCT
6519	Table 3A	NA	193G3	1	TTCAAGGATGTGACTGATATCTGGT TGTTTATTTGTTGTTGGGG
6520	Table 1	NA	194C2	1	AGCTTGGAAATTGAAACAAGGTGGG GACAAAATCAGGAATAACAGACT
6521	db mining	NA	458C8	1	CACTCCTGAGTGTGTTCTGAGAAC AAGGATCAGAGCTTCCGGCTGTGAG
6522	Table 1	NA	458E4	1	TTTCCTTTCGCTGACTTTCCCACTC ACTGCTGTCTCATTTCTCT
6523	Table 1	NA	458G10	1	GCATGGGATTGGCTGTCACTCA TAGCACGGTGATAAACTCAAGGA
6524	Table 1	NA	459B3	1	GTCCACTCAAGTACCTGGCTGTCTA TCTTTGGCTGACCCCTGAAGCGA
6525	Table 1	NA	459D2	1	CTAAGTAAGCAAAGAGGCAGAGGGG AGGAGGGGAGTGTGGTACTGTCC
6526	Table 1	NA	459E6	1	TGGTGCCTGTTCATGATTATTATGC AGGGTGGAAAGTTCAGTATTGGTC
6527	Table 3A	Hs.20830	DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS /cds=(163,2184)	1	AGCACATTGTCAGAAAGCTTGGC AGGTATCTGAGGCACTGCTCACCT
6528	Table 3A	NA	460D5	1	AGAACACACGGGATTGAAGTGGGA AGAGATGGGACCCCTATTGGATCTG
6529	Table 1	NA	460B9	1	GGACAAATAGACCTCTTCACTAGCTC CCTGCTTTGATGGTTGGTTGG
6530	Table 3A	NA	461A4	1	AGAGGATGACTTGAGGTAAATGTT ACGATGCACGGTTAGGCATGT
6531	Table 1	NA	461G6	1	GTGTCCTGGGAGTGAGGAGGGTG GAGTAGACTCTGAGAGGAGTGAAAA
6532	Table 1	NA	461D9	1	AGATCATGCTGGATTGTGTTCCCTA TTACCTAGAGACGAACACAGATCT
6533	Table 3A	Hs.80768	chloride channel 7 (CLCN7), mRNA /cds=(38,2455)	1	GTGTCCTGGGAGTGAGGAGGGTGCA CCATGGACCTCTCCGAGTTCATGAA
6534	Table 1	NA	461H7	1	TGTATGGCTTATAGCCAGAGATGAAA CAGAACCCAAGTTAAATATGCCAG
6535	Table 1	Hs.333513	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating) (SCYE1), mRNA /cds=(49,987)	1	AGGTTTCAGAACATCTGGGCTTACCTT TACAGGTTCAACAAAAGAACATGCCA
6536	Table 1	NA	463A5	1	AAGATGAGGCCTAGCTCATGTACAAA TGCAAGCATTCTCATAAAGTGTCTTA
6537	Table 1	NA	463B2	1	AGATAGTGGTATTGGGTGCTGGGCT TGTCTGAACTGAGGAGGTGGGTGC

Table 8

6538	Table 1	NA	463C5	1	CCTTGCACAGAGACGACTGACATAT ATAGATGGGAGTCACTCATGCCT
6539	Table 3A	Hs.40919	hypothetical protein FLJ14511 (FLJ14511), mRNA /cds=(22,1272)	1	GGTGTAGCGTGAAGATCTGGACAGC GCACTACGCCGGGCCACTGTTTC
6540	Table 1	NA	463H5	1	AGAACGAAACCTGTGAAGCTATAC GTTATCATCAGTGTGAATGCACT
6541	Table 1	NA	463A7	1	TAGTGATAACAATTGGGTGCCAGAG GTTGGGGTAAGGAATTGAGC
6542	Table 1	NA	463B10	1	GTGTGGCCTAAGGAACACCTCTGTG GGGAGTAAGGCCAGCCCTTCCTC
6543	Table 1	NA	463C7	1	AGATGCGGGCGCAAGCTTATGCTCT GTTATGAGGTTAAATTAGATGG
6544	Table 1	NA	463F10	1	TCATAACGCCCTTAAACATTGAAAT AAAATCAGTCGAAACATTGAGCA
6545	Table 1	NA	464C2	1	TGAGAAAGGAGTTAGCAGAATTTAA CATACCGAGAAGCTGTTAGCA
6546	Table 1	NA	464C5	1	CTGGAGACTCAGGTGCTTAAGTGG AGGGACGGGACAGGCCATTCTCC
6547	Table 1	NA	464C10	1	AAGACCTGCCACTTATTTGGCTC TCATCTGACTCTTAAGTGTGT
6548	Table 1	NA	464D8	1	AGACACAGCTGCAGAAAACTTATCT TTCAAGCATGCACAGTCACAAA
6549	Table 1	Hs.221695	7k30d01.x1 cDNA, 3' end /clone=IMAGE:3476785 /clone_end=3'	1	CATTCAACACACAACCGAGCACCT ACTGTGTGCCACGCCACAGACAAG
6550	Table 1	NA	464E7	1	CCTAGGAAACACAGGTCAAAGAAC CAGTCACATGTATTCTAGAAATTC
6551	Table 1	NA	464H12	1	AAACGCAATCTATTTAGGTTGAGAT TAGAAGCTGAGGCCAAGGACTCA
6552	Table 2	NA	465B3	1	TCCCTCAGATGCATGGTCCGTGAAGA AATTAAATAGCAAAGACGAGAAAGA
6553	Table 1	NA	465G2	1	GGCTCTCATGTTATGCCACACATCC TTGATTCTGCTTAAGGAGTCTCTGG
6554	Table 1	NA	465H5	1	AAGCCTGAGCTAACAAAGAGCTGAGG ACAGTAGCTATTCTCTTATGGG
6555	Table 1	NA	465A12	1	TGGATGATGGGATTGGATAAGCATGT GGACTGGATTGTGTTACAAACTCT
6556	Table 1	NA	465F7	1	TGCTGTTCTAGGATTAACACGAAAT CATCACTTTGCCATATTGAGCT
6557	Table 1	NA	465G8	1	GGCTCAGCACAAAGAGAACCGTAG CACTTTCATGTGAAAGCAGACCCA
6558	Table 1	NA	465H10	1	GATATTAAGGTACTTCAGTACAAATC TGGTGTGTAGTGGCTCATCC
6559	Table 3A	Hs.136309	DNA sequence from clone RP4- 612B15 on chromosome 1p22.2-31.1. Contains the (possibly pseudo) gene for a novel protein similar to 60S ribosomal protein L17 (RPL17), the gene for CGI- 61, endophilin B1 and KIAA0491, ESTs, STSs, GSs and two CpG islands /cds=(1011,1406)	1	TCCAGTTCTCATAAACAAATTCTCT ATCCTGGCATTTGGATTGGGTT
6560	Table 1	NA	515C12	1	TCATGGTCATAGCTGTAACCTGTGTG AAATAGTAATCAGATCAAAAGCG
6561	Table 1	NA	516H10	1	ATATGTACCTGGAGGGCGGACGATC GAAATTACTAGTGAATTAGCGGAG
6562	Table 1	NA	55G3	1	TGGGAGTGTAAATTCTGTAAGGAGG TATGGGATAATTAATAGCACGCC
6563	Table 1	NA	55F9	1	GCCCCCAGCATTCATTCAATTCTCTCC CCCTTAGTTAAAGAAACTCTCTCC
6564	Table 3A	NA	99E7	1	AACTTGCTTCTGAAGGTTGGTGT TACCTCGGGCGCGAACACGCTAAT
6565	Table 1	Hs.319825	602021477F1 cDNA, 5' end /clone=IMAGE:4156915 /clone_end=5'	1	ATTGACTCCACTTTGTGCCAAGCTCT GCGGGTAGGCATATTCATATCTT
6566	Table 1	Hs.17481	mRNA; cDNA DKFZp434G2415 (from clone DKFZp434G2415) /cds=UNKNOWN	1	CAGTGGAGAAGCTGCACTGTCTCCG GGCTTGTGTGATCCGATCTCTGTAC
6567	Table 1	NA	116C9	1	AGCTTGAAAGTAATGTCTAACCTG CTGTCACTTATCACAAAGTGCATT
6568	Table 1	NA	128F5	1	AGCTTAATTGAATTGGAGGAGCACCG AACAGGCAGTTCCTGAGCAGTGG
6569	Table 1	NA	135F10	1	GCTCTCACTGATCTCTTCTATCT CTTCTGCACTTATACCAGCACT
6570	Table 1	NA	189F3	1	TGAGAAGAGCTGTGAAGGCAGAGGC GGGGCAAGTGCACAGGCTGACTT
6571	Table 1	NA	189A8	1	AACTCCCTGTTCAAGTTCAAGTTGCTAA TGATCTCAAGCTCTCCCTGATTA
6572	Table 1	NA	195H12	1	CAGCCTAATGCTAACACACAGATA CCATTGGTGGGCCACGTGACCCAG

Table 8

6573	Table 1	Hs.292457	Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds /cds=(498,635)	466C4	1	CACCATCTTTGCTCGGATACTAGCC CGCAATACCCACTCACCTACCCACC
6574	Table 3A	NA		466D1	1	AGGGTCTCCACCTTACAGAAGTACAT GAACAACCAGAGATAGCAGGGCTG
6575	Table 1	NA		466G2	1	ACCAAGGAAAAGTAAAAATCATAGTTG GTGTCTCGGGTTTCACCTTC
6576	Table 1	NA		466H5	1	ATGTATGAGAGAGATTGAGATGAGT TAAAGGAGGGAAAGGGAGGGTGGT
6577	Table 1	NA		466B7	1	CATGAGTATTGGCACTGGGTTCAAG TTCCAGGGCAGAGCAGGATAAGAG
6578	Table 1	NA		466B10	1	CTCCTGGGGCTGGAGTCCTGGTCTG CCTCTGGGGACAGAGATTAGGTCG
6579	Table 2	NA		466C9	1	TGGAACCTTCAGTCAAAAACATCTGA CTTTGTACAGGACAAAGATTGGC
6580	Table 1	NA		121F1	1	ATAGAACTTGTTTACCTATGAGCCTT GCCTTGATTTTACTGATGTGGC
6581	Table 1	Hs.7187	mRNA for KIAA1757 protein, partial cds /cds=(347,4576)	121A11	1	ACATCTCTGAAAGTCAAATGTTA CAGCAAGGTAAACACTCCACT
6582	Table 1	NA		121F8	1	GGGTGAATTAACTGGGAGATGGGTA GTCAAGGGCAAATGATGGGTGGTT
6583	Table 1	NA		178B2	1	TGCAATTGAGACAAATTGTTAGA GTTAAATCCTGGCTGTTCCT
6584	Table 3A	NA		178B5	1	GGACCTATGTCCTCAAGACATGGAAA CTACTAGTTCTGCTGCGCAGGAG
6585	Table 1	NA		178F5	1	AATTAAGGATCCCCTACCGACATCTA TCAGCATACCTGAACAGGTCGA
6586	Table 3A	NA		178C12	1	CGGCCAACCCAGGAGGGCAGGTGTT TTGGGCATCTGGTTTATAGTACCTC
6587	Table 1	NA		462A11	1	GCTGGGGTAAAACCTGAAGACTCA GACCTCAGTGGAAACAGATGAATGT
6588	Table 1	NA		462D9	1	CCCCCAGGCTCTGTGACGCTTGAATT CTAATTAGCGCAGAAAAGGGCTAA
6589	Table 1	NA		462E8	1	CCTGACTACGTGTTTCCCCACAGAC ATCACACTGGTTCACCTCGTTGA
6590	Table 1	Hs.13231	od15d12.s1 cDNA /clone=IMAGE:1368023	462F9	1	AATGGAAAGACACTTCTGTATAACT GGAAATCTCAGGAAATTCTTTTCC
6591	Table 1	NA		462F11	1	GACAGTACAGTACCCCTAACGACTG AGGAGGGCACCCACGTGAAC
6592	Table 1	NA		462G12	1	TTCCCTGGAGATTTCAGGCATCTTA GGCCGGAAAGGGACCTCGAAGGTT
6593	Table 1	NA		462H9	1	CTCCGCTTCTTCACTCATTGTTAG TGTTCCTTAAGCTTGTGCTTGT
6594	Table 1	NA		472B1	1	TCCACATTGATCATGCATTATGAA AGCCCTGGGTTTGTATTGAGAA
6595	Table 1	NA		472C1	1	GCTATCTCTGCTGAATCAGCGTAAT GCTGATATACACCCCTATTTCTGT
6596	Table 1	NA		472E6	1	AAAAGAAAAGTTTCAACCCAGGA ATTATAGTGGGTGTCAGTCGAGA
6597	Table 1	NA		472F4	1	AGGAGACGATGTAGGGGAAGTGTG TTAGATTGTAATGGAGGGTTTGG
6598	Table 1	NA		472G2	1	GCTCTTCCCAGACCCAGGCCAG GTTCTGTAGAAAGAAAATAATGC
6599	Table 1	NA		472D7	1	AAGGGAGGAATGGGAATCTCAAGCTCA AGGGCACTCTCACTAATTGTGGT
6600	Table 1	NA		472G12	1	AAATAGCCACCTTCTCCCCATTCT GTCAGAACACACACTTATATCCA
6601	Table 1	NA		472E5	1	TTTGGAAAAGAGATTGGAGGGGACA CCAGGGAAACAGGATTCTGGC
6602	Table 1	NA		472D9	1	AAAGTGTAAAGGCACTCTCTAAACTAT CTTCCAGCTCCGGGCGACAAATGG
6603	Table 1	NA		472F5	1	CCACTCTCTAACGTCAGCGAGTCCTT CCTGCATACCTGACTGGGTGCTG
6604	Table 1	Hs.75354	mRNA for KIAA0219 gene, partial cds /cds=(0,7239)	64G9	1	GGACTTTGCAGGCTTCATCCCTGTC TGTGTCTTCTCTGGTGTGTT
6605	Table 2	NA		467E5	1	ATTGCTGGCCAATCCTGCTGACTAT GAATCTTGGGGCACTGAGTTAC
6606	Table 1	NA		487A8	1	CTGGGGTACTGGGAAAAGGAACCTG GTATTGAGATTATTTGGGGCG
6607	Table 1	NA		467C9	1	TTGAGTAAGGCTCAGAGTTGAGATG AGGTGCAAGAACACCTCTGTGACT
6608	Table 1	NA		467F8	1	GGTCACAGAGAAGAAATGGTAGCTGA AGAAGCAGGGCACGAGGGCTAAC
6609	Table 3A	NA		468E6	1	TTTCCGGTATATTGTTGTTGTTGAC TTTTGTTGTTGTTGTTGTTG
6610	Table 1	NA			1	GGATCTCTGCTCTCACCTGTGT GACAGACTAACAGCCCCAACTG

Table 8

6611	Table 1	NA	468B9	1	ACAGTGTGGGACAGAAGAGTCCTCA GTGATTAATGCCTGATAATAGATT
6612	Table 1	NA	468E10	1	CTCTCTCGCAATTACAACCGCTTC AGTACCATTCACCGTCACTCCCT
6613	Table 1	NA	468F10	1	CTTTGGGAGTGGAGTTGTTAGAT GGGGAGAGAAATCAGAACAGGAGA
6614	Table 1	NA	468F11	1	CCTTACTGCTTACGGTCATGGTCAT CAGCCCAACCCGCTGGTAGGT
6615	Table 1	NA	468G12	1	AGAGTATAATTCCCCAGTGGAGT GGTTAGTGTGCTAAAGAAGAGGT
6616	Table 1	NA	468H11	1	CTGATGTCGTGCTGCACTCACCTGG TCATGTGTTCTGTTGCGGTAGT
6617	Table 1	NA	469B6	1	AGGGGAGAGAAAGAACACTCA CAAGAGATGACCAGGAGTAAACTG
6618	Table 1	NA	469D2	1	CCAGCAGAGGCCAACAGCAGCA TACCCAACCTCAGCCAATAAAA
6619	Table 1	NA	469A10	1	TGTCAAATACGGCGAGAAGAAGTG CATGAGAAAGTGTATAAGCTGT
6620	Table 1	NA	469E12	1	CCAGCTTTCTTGTGTTAGTTAG CAGTAAGTCACAGGTTGAGCACC
6621	Table 1	NA	469F8	1	GGCACGCATCTCATTCTGCATGCT CTTAAATATCTATCAATGATCAT
6622	Table 1	NA	469G8	1	ACTCTATACTCAGTGCCTGTGGGT AACCAAGCAGCAGGTTGTC
6623	Table 1	NA	470B2	1	GCCTAGAGCATGAATAATTGAAGA AGGTAGACTATTAGCTGGAAGCATHC
6624	Table 1	Hs.118174	tetratricopeptide repeat domain 3 (TTC3), mRNA /cds=(2082,7460)	1	CAAACAGGGGATTAAAAAAACTCA AAAATGTAGTTAAAACCTCTCACTTAA
6625	Table 1	NA	470C3	1	GAAGGAGAAGATCTGAGTAACCCCA
6626	Table 1	NA	470D5	1	ACCTGAACAATGAATGAAGAAAGGAA GACTTGGTCTCTACCTCTGGAC
6627	Table 1	NA	470E1	1	CATGGCTCACAGCTCTAACACTCCC CTCCCTCCAGATCCTAAGAAGAAG
6628	Table 1	NA	470E5	1	TCTGAGCTTCACCTCAAGAACCTGTA GTCCTAAAGAACCTGGTCTTCAG
6629	Table 1	NA	470F3	1	ACTTCACTCACTTTAGCCTGTTCAT ATGAGCTTGTCACTGCTTTGTT
6630	Table 1	NA	470G6	1	TGAGGAGGATGGGAGGCCACAGGC AATTAGCTAGATATAGAAAGAGAA
6631	Table 1	NA	470B8	1	AGCTGATTTGGATTCTGGCTTTC ATCGGCTTAATTCAAGTGTGT
6632	Table 1	NA	470G10	1	TCACATCTGGAAAGCTTCTACATA TCACACTACTGGCTCACCTACTAT
6633	Table 1	NA	471D6	1	TAGCACTGAGCCAGAGTCCTGCTT GTACCAAGGAAGCTGGTGGTGGTT
6634	Table 1	NA	471F1	1	TGGATAGTCAGAATTACGTGTTTGT GGATTGGGAGGGAGGGAGGAAA
6635	Table 1	NA	471F4	1	GCACTCTGGAACTTCTACATAATT CGGGGACAGTTTGTGAATGTTG
6636	Table 1	NA	471F6	1	TTGCTCGGGATGACCTGACTGAGCC CTGGGAGACTGTGCTATAATCTCTC
6637	Table 1	NA	471E9	1	AGAAGGAGGATCTGTTCTAACATCT GCGAGGGGAGGACAAAGCATTGAA
6638	Table 1	NA	471E11	1	CTTGATCTGAATGAGATGAAACCTT TCTTCCCAGCCTGAGAGAGGGA
6639	Table 1	NA	471H11	1	GTCAGCTGGCAAGTGTGATGGATGAAT GGATGAGCTGGCAGACCAACAGAA
6640	Table 1	NA	473E4	1	TGCAATGAAATGTTGAGTACGGGG AAAATAAGGGAGCaaaaACTGTGT
6641	Table 1	NA	473F3	1	TTTAAGGTGTGACTCAATTACAGG CATTCTGTATTTTGCATTTGGT
6642	Table 1	NA	473E11	1	ACCTTGGGAGAAAGTCTTACAACTA CATGAAATGCAATTATGGACTC
6643	Table 1	NA	478C1	1	GAAGGGACAGAACAACTCAACTGTGA GAGATGGAAGAAAACCTCAATGGA
6644	Table 1	NA	476D3	1	CTAGTTGGGACTTCTTATTGGGCAC GTGAATCCAGGAGGGCTGAATT
6645	Table 1	NA	476F5	1	GGCCCAAGATTGTAGACAGCATAAAA TAATTGGGCTTTCTGTAA
6646	Table 1	NA	476G3	1	CTGGGCTTCTTGTGAGAACGCC GCAGCCAAGAACAAACCAAGTGCACACT
6647	Table 2	NA	476G4	1	GAAGGGGGATTCGGTGATGGGGAA GCAAGGGACAAGGGAAAAGGAAA
6648	Table 1	NA	476A10	1	AACCCAACCATGAAAAAGAAGAAGCT CTGGACTACGGCCAGCGTGGGAG
6649	Table 1	NA	476G8	1	TGGCTATTGAGTTCTCTTACATGA AATGCGCTGGCAACGTACACTGGC
6650	Table 1	NA	476H10	1	TGAACCTGATTCCGCCAACACTAG GAGGAAACACCCAAAAGAACAGCG

Table 8

6651	Table 2	NA	477E1	1	TTTGCTGGGACTAAAATCAAACACTGC ACTGCAGAGCAGGTGAGGGTCAT	
6652	Table 1	NA	477E8	1	TGGAGAGTGTGTATTACCATTTTT TACATTCATCACATTTACCATCTAT ATCT	
6653	Table 2	NA	477A11	1	TTTGAAGCCCTCATAGAGAAAGAC TGTACCATAGAGAAAGCCCCTCA	
6654	Table 1	NA	477D9	1	AACCTCTAGTCATGAGCTTGATTAC TCCATTGTACCATTTGGAAAGCCA	
6655	Table 1	NA	477D10	1	GTGGGTAGCCATTAAGTGGTCTGGC ACAGAAAGGGACAAGTAGCTTCAG	
6656	Table 2	NA	480A3	1	CTGGTGTAGTGGAGTACAGTAA GGCTGTAGATGGAGCGCCCTGGGAA	
6657	Table 1	NA	480B5	1	TTTTGATGTGACCAGTCGTGATGGC GGGGGACAGGAGCTAGGGGAAT	
6658	Table 1	NA	480D2	1	ATTATGCATGTGAGGGGACAACATT TATTAACAGGAGGGGTGTGCTT	
6659	Table 1	NA	480E2	1	TGGTCATGTTCCCTCTTACTCCAC GACAGTTTCAATTGTAACAGG	
6660	Table 1	NA	480E3	1	TTCTGTTGTTATATGAATGGCAGTT ATTGTCTCCCACTGTGTTGGGTTCT	
6661	Table 1	NA	480F3	1	AGTCCCTGGCAACTTACCTGGGAATT GTCTGTAATCTTAAAGCAGTGGCG	
6662	Table 1	NA	480G4	1	AGGACTTATCTAGCTTCACAGATT AGAGTGCCTTCAACATCATTG	
6663	Table 1	NA	480C8	1	TTAACACGGCTTATCTAGGACATAGG CCCAAGAGGGAGGGAGGAGGAAGGC	
6664	Table 1	NA	480D9	1	CTCAGGCGCAACGAGCCTCACTC TGGATTAAGATCTGTCATCTTGACA	
6665	Table 1	NA	480E7	1	GCAGGACTTGTGGCAGGACTCAACG GGAGAGAAAGAGGCTGAAACATAAA	
6666	Table 1	NA	480E11	1	AAGAACATCCCAACTTTCCGGTAGG CAAGTGTCAAGTCACCTGGACAAAT	
6667	Table 1	NA	480F8	1	TCTGTGGCTTGTGTTGGGACCTGC GCCCTTTAAATTAGGGCATATTAA	
6668	Table 1	NA	487F11	1	GGCCTAAAACCTGGTATTAAATGA CAAACAGAACGTGAGAAGAGATT	
6669	Table 3A	NA	499G1	1	TCCTGCACACAACAAATAAGACAAG AATAAAGGGCACCCATCAGTAGC	
6670	Table 1	NA	518F10	1	ATGTTGTCAAATTAAACATCATACCA CATGGGGCAGCTACCAATT	
6671	Table 3A	NA	524A12	1	TAATATGAAAAGCTGGAAAAGAATTA AGGGGTTAGGGAGACGTGCCCCGT	
6672	Table 1	NA	526B9	1	GTACCCCTGACGAATCGAGTCCTCGT GTGGAATGTCATGCCCCCTTGAG	
6673	Table 1	NA	583B5	1	ACACCAAGCAGTCATAGGGAAAGGG GAATACAGTTAATTGGGTATTGTT	
6674	Table 1	NA	583D8	1	ACTCCCTCCCATCTCTGGTCTTAGT TGGAAAGCAAGCTTTCGGACAACCG	
6675	Table 1	NA	583G8	1	TCCAACAAGGGTACGGCAGAATTAA TGCAGAAAGTCTCTTGGCTAAA	
6676	Table 3A	NA	584A1	1	TTGTTCTGTCAGGCAAGGATTGTT GTGTGCTCTGTATTGCTGCTT	
6677	Table 1	NA	584D3	1	GGCCCGCATGCTTCGTTTGTCAG TCCTCATCCAATCCATCTTAT	
6678	Table 3A	NA	DNA sequence from clone RP4-620E11 on chromosome 20q11.2-12 Contains t		1	GTGGGTTTTAGACACCTGCAGCAAG AAGAAATCTGACTGACTAGGCAT
6679	Table 3A	NA	591H9	1	TTTAAAGAAAAATCTATTATCTTGGG GCATGGATGGGGAAATGCGAAGG	
6680	Table 3A	Hs.6179	DNA sequence from clone RP3-434P1 on chromosome 22 Contains the KCNJ4 gene for inwardly rectifying potassium channel J4 (hippocampal inward rectifier, HIR, HIR1, HIR2, KIR2.3), the KDELR3 gene for KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3, the DDX17 gene for DEAD/H (Asp-Glu- Ala-Asp/His) box polypeptide 17 (72kD), ESTs, STSs, GSSs and six putative CpG islands /cds=(307,2259) 602388170F1 cDNA, 5' end /clone=IMAGE:4517129 /clone_end=5'		1	CAGAAGAAACATGGCAAACCTGCTG TGCTTCAACACAAAGTGTCCCC
6681	Table 1	Hs.44577	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN 119F12		1	GTTACTTAAGATCAGTATGTGTTGGTG CATATGTGATTCGACCATTCAGT
6682	Table 3A	Hs.108124	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN 119F12		1	GAGAATTTCGCTGATCTATGACAC CAAGGGTCGCTTGTGCTGACCTCG
6683	Table 1	NA	119G10		1	CTGGGTTAAACTCACCACATTGAG AAGGTGGTCTGCTTGTGTA
6684	Table 1	NA	119G10		1	GGAAAAGACAGGTGAGTGTGCCACAA CTACCTAACACATCAGCAAATCTGG

Table 8

6685	Table 1	NA	485A6		1	GTCACTTTAGCGAGCGGGAAAACAAT GGCGGAAAGGGAAAACCTGGAAAG	
6688	Table 1	NA	485D5		1	CGATAAGCTGTGGTGTGGGAGTGA GAGATGTTACTTTGCGAATGTTCAA	
6687	Table 1	NA	489H9		1	AAAGGCTAGGTTGCGAACGCCCTC TAAACTATGTTGGTGGTACT	
6688	Table 2	NA	494B11		1	CTGACCCCTGCAGGGCGGAAGATAAA ACAAAAACGAGAAGAACAGCAAGA	
6689	Table 1	NA	478E5		1	AAGATTGAAAAATACATTTAGGCTC AAGAGTCCAGGGGTTTCAGAGC	
6690	Table 1	NA	478G6		1	TGCAAGCTGCACCTTCACGTTTATT TTAAAGGGCTTCACATCAAAGAT	
6691	Table 3A	NA	478H3		1	AAACAAAGAAGGGAAATGAAGAGGG GGAAAAGATGAACATCAGGCTGGGT	
6692	Table 1	NA	478C7		1	TCCAAGAGATGTTCTGGTGTTCAGC ATGATTCTGGTGTAGTCTTTCT	
6693	Table 1	NA	478G8		1	TTTGTGGGTGCGTGAGAGGGGATTAA TACTCCTTGAGCCATATTGTTGTA	
6694	Table 1	NA	478H7		1	GGGTTACAGCATGGGTGGAGGTA GTAGTATTCTCATGGTTGGTTAGT	
6695	Table 3A	NA	478B4		1	GACAGTGAGAAGAATATGGAGTAGA GTCCTTTGGTCTTGAGGCGGTCA	
6696	Table 1	NA	479D2		1	AACAGCTGAAGAACAGAACAGGTGAG CTCTGAATGCGTCAGGTGGTCATT	
6697	Table 1	NA	479G2		1	GGCTGACCAGTACAGGCTTGGGAAT TTATGTTGGTGGTTCTACCAA	
6698	Table 1	NA	479G3		1	GGGGGAGCTATAATTACTGATTAAAC CACCATTTCTCACCCAACTTATG	
6699	Table 1	NA	479G5		1	AAGTCTGTATTATGAGGTACTIONGG CTCTGGGGATATTGAGATGAGAA	
6700	Table 1	NA	479G8		1	AGTCCCTGCTGAATCATTGGTTATAG AAGACTATCTGGAGGGCTGTAG	
6701	Table 1	NA	479H4		1	GGAGCTTCCAGCTTAATAGAAAAGAT GCACTTACGAATAGACTTTGGGTA	
6702	Table 1	NA	479H5		1	TCTGTGCTCTGGACCCGTACCCCT GAGCTCTCAGTTGCTGAACCATC	
6703	Table 1	NA	479H6		1	TGCTGGCATGTGGATAGACTTTAGCA AATGGTAGTCATCTCTAATTCT	
6704	Table 1	NA	479G12		1	AATGGGAATCTTAAGGCCTCTCGGA AAGGGTGTGAGGGGGTCGAGGGGG	
6705	Table 1	NA	479H12		1	TGCAATTGTCACTGACTGGCTAGGG TCTCTAAATTGAAACCTTACA	
6706	Table 1	NA	482A5		1	GTCAGCAACTAAAAGGGAGATATAT CTTAGAGAGACTTGAATAAGCAACTC	
6707	Table 3A	NA	483G5		1	GGAAGGACTCAAATGGCCATAAAG GCAATACGGCATGTTCATTACACCA	
6708	Table 1	NA	486C4		1	TTTGTGACTATGAAATAGTGGTCT GGTTTAACTCTTGGGTTCCCT	
6709	Table 1	NA	490F10		1	AATTATATTAGGCTGATGTGGGTG GTCTGTAATGCTCTCATTTACAC	
6710	Table 1	NA	493C2		1	CTGTGTTCTGTATGGTATTGCAATTG TCCCGCCCTGGGGTTGGTGG	
6711	Table 1	NA	58G4		1	TTCATGCTCATTAGGACATTGAACAA ATGGCAGAGTAAGAAAAGTTGGCC	
6712	Table 3A	Hs.169370		DNA sequence from PAC 66H14 on chromosome 8q21-22. Contains FYN (P59-FYN, SYN, SLK) gene coding for two isoforms. Contains ESTs and STSs /cds=(12,1706)		1	GGAAATGGACTCATATGCAAGATTG TGACTTCGGATTGGCCGATTGAT
6713	Table 1	NA	598H2		1	CAACACATGGGACGGGAAGGAAATC CTTCGCGTGATTTGTTAAAAATA	
6714	Table 3A	NA	AA077131	1836605 7B08E10 Chromosome 7 Fetal Brain cDNA Library cDNA clone 7B08E10, mRNA sequence		1	CAGCCACCTCCTCAGGTAGACAAG CCCAGCACCCAAATACCACTATCTG
6715	Table 3A	NA	AA501725	2236692 ng18e12.s1 NCI_CGAP_Lip2 cDNA clone IMAGE:929806 similar to contains Alu repetitive element, mRNA		1	GGCTTCCCTATTACCTCCCAGCGAAA TTCGTAGTCTCTATGGAGTT
6716	Table 3A	NA	AA501934	2236901 nh56a10.s1 NCI_CGAP_Pr8 cDNA clone IMAGE:956346, mRNA sequence		1	TGCTGATGTGTTAGGTAGTTGGCA CACTCACCTGTCCTTCTAAATGC
6717	Table 3A	NA	AA579400	2357584 nf33d05.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:915561 similar to contains Alu repetitive element;contains		1	TTCATGCTCAGCAAAACACGTTTAA GGATGGTAGAGAGAACAAAGTAA
6718	Table 3A	NA	AF249845	8099620 isolate Siddi 10 hypervariable region I, mitochondrial sequence		1	TATTAACCACTCACGGGAGCTCTCCA TGCATTGGTATTTCGTCTGGGG

Table 8

6719	db mining	Hs.277051	AI630242	4681572	ad07c09.y1 cDNA /clone=ad07c09-(random)	1	TTACCTGTTGCATGCTCTCCATCG
6720	db mining	Hs.277052	AI630342	4681672	ad08g11.y1 cDNA /clone=ad08g11-(random)	1	TCAAAGTCTCTGAAACTTAGGC
6721	db mining	NA	AI732228	5053341	nf19e05.x5 NCI_CGAP_Pr1 cDNA clone IMAGE:914240 similar to contains Alu repetitive element; mRNA s	1	CCCCACCCCAACACATACAAACGTT
							CCCAACATCCTGAACTGCAAAA
							TTCAAGGTCCAATACCCAACTAAC
							CGAAGGAAGAAATGGAAATCTATT
6722	Table 3A	Hs.197803	AW379049	6883708	mRNA for KIAA0160 gene, partial cds /cds=(0,2413)	1	TGCACAGAACTCTTACTTACATGTCT
6723	Table 3A	Hs.232000	AW380881	6885540	UI-H-BI0-p-abh-h-06-0-UI.s1 cDNA, 3' end /clone_end=3'	1	CATCGAAACTCCAGAACACCGTCTG
6724	Table 3A	Hs.325568	AW384988	6889647	602386081F1 cDNA, 5' end /clone=IMAGE:4514972 /clone_end=5'	1	TGCATGTATCCCGTAATTCAAATCC
							AATTTCACAGGCCACTGCTGAATAT
6725	Table 3A	NA	AW836389	7930363	PM0-LT0030-101299-001-f08 LT0030 cDNA, mRNA sequence	1	TACAGGAAAATGAAACTAGACGGGTG
6726	Table 3A	NA	AW837717	7931691	CM2-LT0042-281299-062-e11 LT0042 cDNA, mRNA sequence	1	GGGGACACTAGAATGAAAACCAAGT
6727	Table 3A	NA	AW837808	7931782	CM1-LT0042-100300-140-f05 LT0042 cDNA, mRNA sequence	1	AGTTTCTGCTTCAGTGACTGAGGCT
6728	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence	1	TTGCTTAAACCTGGTGACTIONCCA
6729	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	1	AATCACTAATTCTGGAGCACAGGA
6730	Table 3A	NA	AW856490	7952183	PM4-CT0290-271099-001-c04 CT0290 cDNA, mRNA sequence	1	CATGGATGGGGCAGTGGTGTCTCT
6731	Table 3A	NA	AW891344	8055549	PM2-NT0079-030500-001-a04 NT0079 cDNA, mRNA sequence	1	AGTGTGTAGGGAAAGCAGCAGATG
6732	Table 3A	NA	BE061115	8405765	QV0-BT0041-011199-039-f09 BT0041 cDNA, mRNA sequence	1	TGAAACAGTCTATAATCACAGA
6733	Table 3A	NA	BE086076	8478469	PM2-BT0672-130400-006-h09 BT0672 cDNA, mRNA sequence	1	CAGACGCTCAGTGGCTCCGAGGTT
6734	Table 3A	NA	BE091932	8482384	IL2-BT0733-130400-058-C11 BT0733 cDNA, mRNA sequence	1	ATGTTGTTATTAGACCTGAAATGA
							CCCTTAAAGCCTTGGCCGAAACAGT
6735	Table 3A	Hs.173334	BE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922)	1	GAACACTAAATAGATATCCTAACAGT
6736	Table 3A	NA	BE163106	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence	1	ATGGGGATCATGTTTATTTCTCTA
6737	Table 3A	Hs.301497	BE168334	8631159	PM2-BT0672-130400-006-h09 BT0672 arginine-tRNA-protein transferase 1-p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544)	1	TATAATGGGCCAGTGTGTTCCA
							ACCTGTAGACCATAAGCCACCTTCAG
6738	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453466 /clone_end=5'	1	GTAGTGGTTGGAAATCAAGCAA
6739	Table 3A	NA	BE177661	8656813	RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence	1	ACTCAGCAGTAACTCCCAGTAGGA
6740	Table 3A	NA	BE178880	8658032	PM1-HT0609-060300-001-g03 HT0609 cDNA, mRNA sequence	1	AAGATTCTAAAGGAATAGTTCTT
6741	Table 3A	NA	BE247056	9098807	TCBAP1D6404 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA cDNA clone T mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	1	GATGGTCAGGCACAGGTAGAAATCAA
							TCTCTGTATGTATGTTCACACAGA
6742	Table 3A	Hs.11050	BE763412	10193336	MR0-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	1	TACCTGAAGGTGTAGAGAGTCCCCG
							CATCCAGCAAGGCCAACAGCTCCAC
6743	Table 3A	NA	BF330908	11301656	RC3-BT0333-310800-115-f11 BT0333 cDNA, mRNA sequence	1	CTGTGTTTCCCAAAGCAACAATTTC
6744	Table 3A	NA	BF357523	11316597	CM2-HT0945-150900-379-g06 HT0945 cDNA, mRNA sequence	1	AAACAAAGTGAGAGCCACTGACA
6745	Table 3A	NA	BF364413	11326438	RC6-NN1068-070600-011-B01 NN1068 cDNA, mRNA sequence	1	GACTCCGAGCTCAAGTCAGTCTGTAC
6746	Table 3A	NA	BF373638	11335663	MR0-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	1	CCCAAACCCCTAACCCACTGCTAC
6747	Table 3A	NA	BF740663	12067339	QV1-HB0031-071200-562-h04 HB0031 cDNA, mRNA sequence	1	TGTAACTGACTTTATGTTCTACCAAG
6748	Table 3A	NA	BF749089	12075765	MR2-BN0388-051000-014-b04 BN0386 cDNA, mRNA sequence	1	TCTCTCTAACAAAATGTAATCTTC
6749	Table 3A	NA	BF758480	12106380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	1	GGACAGCAAACCTGGAAGCTACTATC
6750	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	1	GTGTTTATCATCAGTGTGAATGCACT
6751	Table 3A	NA	BF773393	12121293	CM2-IT0038-191200-638-h02 IT0039 cDNA, mRNA sequence	1	TTCTGCTCTCATGTCGGTGA
6752	Table 3A	NA	BF805164	12134153	QV1-CI0173-081100-458-f03 CI0173 cDNA, mRNA sequence	1	AGCGTGTGACATCTTCAGCCATGTT
							CAGGGTTAACAAAGTATGGAATTCA
6753	Table 3A	NA	BF818594	12156027	MR3-CI0184-201200-009-a04 CI0184 cDNA, mRNA sequence	1	ATTCTGTTATGCTGCAGCCATGTT
							CCT
							TGTAATTGATTCGGCATAAACGGTC
							ATTACTGGCACCATGGCAGCACC

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6754	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08 HN0025 cDNA, mRNA sequence	1	GTGATCCACTTGGAGCCTGACTGGT CCCATTGAGTCCTATAGTACTTCA
6755	Table 3A	NA	BF845167	12201450	RC5-HT1035-271200-012-F08 HT1035 cDNA, mRNA sequence	1	TGCCATGAAATCTCTATTAAATTCTCAG AAAGATCAAAGGAGGTCCCGTGT
6756	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119 cDNA, mRNA sequence	1	CCACCTGGAAATCCTCAAGTGTGA CCCTAGTCATTTCTCCCTTTGG
6757	Table 3A	NA	BF875575	12265705	QV3-ET0100-111100-391-c02 ET0100 cDNA, mRNA sequence	1	GCTAAACAGAAAAGAACCTGAAGTAC AGTCCCGTCTTCAAAGAAGATGC
6758	Table 3A	NA	BF877979	12268109	MRO-ET0109-171100-001-b02 ET0109 cDNA, mRNA sequence	1	ATCCCTCCCTCCCTGGATGGCATAGA AGAGACTTTAACCAAAATGAGCC
6759	Table 3A	NA	BF897042	12288501	IL2-MT0179-271100-254-C11 MT0179 cDNA, mRNA sequence	1	GTCAGTAAGCTCTGCCCTCCAAGAAG ACACAGTGAGAGGTGCCCCAGTC
6760	Table 3A	NA	BF898285	12289744	QV1-MT0229-281100-508-e11 MT0229 cDNA, mRNA sequence	1	GTTCACCTTGTACTTCTCTCACC TGCTGTGAAGCTCTGCACCCCTGC
6761	Table 3A	NA	BF899464	12290923	IL5-MT0211-011200-317-f03 MT0211 cDNA, mRNA sequence	1	AGAGTAATCCACATCCAGGGACAGT CACAATGACCTACGGCTTAGCTG
6762	Table 3A	NA	BF904425	12295884	CM1-MT0245-211200-662-d02 MT0245 cDNA, mRNA sequence	1	CGAGGGCTACACCAAGTCCATTGATA TTGGTCTGTAGGCTGCATTCTGG
6763	Table 3A	NA	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	1	TCTTCTCTAAAATGCCCTCCCTCCCT CCTTTTCCAGACCTGGGTTAAA
6764	Table 3A	NA	BF926187	12323197	CM2-NT0193-301100-562-c07 NT0193 cDNA, mRNA sequence	1	TGCCCATTTGGTAGTCCACAGTGAC TGCTCTCTATTTACGAAGCCAC
6765	Table 3A	NA	BF928644	12326772	QV3-NT0216-081200-517-g03 NT0216 cDNA, mRNA sequence	1	GTAGATTACTATGAGACCAGCACCT CTGCTCCAGCCAGCTGTGGTGTG
6766	Table 3A	NA	BG006820	12450386	RC4-GN0227-271100-011-d03 GN0227 cDNA, mRNA sequence	1	TTTCTTTTCGCTGACTTCTCACTCA CTGCTGTCTCTCATTTCTCCA
6767	Table 3A	NA	F11941	706260	HSC3F051 normalized infant brain cDNA cDNA clone c-33f05, mRNA sequence	1	TGGTAAGTTCTGGCAGTGTGGAGAC AGGGGAATAATCTCAACAGTAGGT
6768	Table 3A	NA	U46388	1236904	HSU46388 Human pancreatic cancer cell line Patu 8988t cDNA clone xs425, mRNA sequence	1	CCATGGTGGTGTGACTTGTGTTG GGGCTTAATCCTAGTATCATTGG
6769	Table 3A	NA	U75805	1938265	HSU75805 Human cDNA clone f46, mRNA sequence	1	TCAGTGGGTGTTGGTGTCCATTAGT TGAGACTTAGTTGCTGCTGGGA
6770	Table 3A	NA	W27656	1307658	36f10 Human retina cDNA randomly primed sublibrary cDNA, mRNA sequence	1	GGCTGGACAGCAGATGATTCAAATCT CAATACTACATGCCATTCTGTGG
6771	Table 3A	NA			36G5	-1	CAGGATGGAACAAGACTCCAGCCCC TGCCTGTCTCATGTATCTGCAAGGG
6772	Table 3A	NA			36F11	-1	CTTCAGTGGCTACAGCAGCTAACGT TAGTGGCAGGAAGACAACTACTC
6773	Table 1	NA			37G7	-1	ACTCGTATGCCAACTCTCTGTCTC ACTACTAGAGTGTAGATTGGACTC
6774	Table 1	NA			37G8	-1	TGGACTGGAACTTGACTGAAAGTTAT GTGGCTTAATGAGTAAGTTGAGCC
6775	Table 3A	Hs.197345			thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA /cds=(17,1846)	-1	ACTGGTTATTGTTCCCGATAGAG CTTTATGGAGGAGGCTTGAGAGC
6776	Table 1	NA			40E4	-1	ACCATCTCTTAACTCTCACAGTGA TCCTGGAGCAATGTGTGATTCT
6777	Table 3A	NA			41E9	-1	CATCACCTGTCACCTAGGAACCAGG AGTACTGGGAACCTGTTCCGTTACT
6778	Table 3A	Hs.169476			Homo sapiens, glyceraldehyde-3- phosphate dehydrogenase, clone MGC:10926 IMAGE:3628128, mRNA, complete cds /cds=(2306,3313)	-1	TCATTGCTGATGATCTTGAGGCTGTT GTGGAACCTCTCATGGTTCACACC
6779	Table 3A	NA			47E5	-1	TGGCACACGCTGATTATTTCTTTT CAAATCCCACCTATACACCTCC
6780	Table 2	NA			47D11	-1	GCTGTCTGTTCCCAATATCCATGA CCTGACTGATGCAAGGTGTCTAGG
6781	Table 1	NA			50A11	-1	AGGCCTTTTATTTGTCTGTTAGATA CACTGCTTCTATATCTGCTGGA
6782	Table 3A	Hs.132906			DNA sequence from clone RP11- 404F10 on chromosome 1q23.1-24.1. Contains the 5' end of the SLAM gene for signalling lymphocytic activation molecule, a SET (SET translocation (myeloid leukemia-associated)) protein pseudogene, the CD48 gene for CD48 antigen (B-cell membrane protein), the gene for a novel LY9 (lymphocyte antigen 9) like protein and the 5' end of the LY9 gene. Contains ESTs, STSs and GSSs /cds=(41,1048)	-1	CCCGTCCCCACAGCTCACTGCC TGACTCCAAGTCTCGTACACTAGAT
6783	Table 1	NA			52B9	-1	AGCGATGAACTGTTGCAAAGAATT TCCAGAGCATTTCCTTAAACCA
6784	Table 1	NA			53B1	-1	CCATATTCTGTTCCCCAGCCAGGTG CTGCACCTCCCCACTCTTTAGTG
6785	Table 1	NA			53E3	-1	AAATGCTTAAAGGAACAATATATGTC CCTTCGAGGACAGTGATTGTT

Table 8

6786	Table 1	NA	53E10	-1	TCTGGAGCCACACCCCTTACCATCACC TTCCAAGAAGAAATTGAAACCTT
6787	Table 2	NA	53G7	-1	AATCACACAAGGTCGAAAAGTAGACAG TCCTCTGGACTTGGAAATTGTCCA
6788	Table 1	NA	54F4	-1	ACTTTCTCGGGAAAGTTGTATCTT AGCGTGGACAACAGGTTAACCAA
6789	Table 1	NA	54G9	-1	TCAGGATGCTCACTTTAAGAACCG GGCAAATAATAGAACACTGTGACA
6790	Table 1	NA	59G1	-1	ACTTCACTCAGAGTAATGAAAAGAC TGGGTGCCTCATCAATATCATTGT
6791	Table 1	Hs.48320	mRNA for ring-IBR-ring domain containing protein Dorfin, complete cds (cds=(317,2833))	-1	TGACTGAAGGCAAGCTCACAGATGAA GCAGAGGACTGAAGATCTGATCT
6792	Table 1	NA	60G8	-1	GCTGAGAAGGATGTGGTATAAATGTA TTAACGAGCTTAGGGTCTGGCC
6793	Table 2	NA	62C9	-1	AAGTCCCCGCTAGTGGGAAAGAAA GAAGTTGAACAAGTAATTCCAAGGG
6794	Table 3A	NA	62F11	-1	CGCCCGGCAAGTACTGGGTTCTTA TAGCTTCTCTGCATCACAAAG
6795	Table 1	NA	63E1	-1	CTGTTCTCTATTTAACTTACATTGG TTATTCTGAAAGTCAGATGTGGCAG
6796	Table 2	NA	65B1	-1	GCACGTGCCCTCCCAGTCTACATTT GAGTCGAGTTGACTCGCAAGACT
6797	Table 2	NA	65D10	-1	AACAGATTGTGCTTCTGAAATC TTCTAAAGCCATCTGCACAGTGCT
6798	Table 2	NA	65D11	-1	AACAGATTGTGCTTCTGAAATC TTCTAAAGCCATCTGCACAGTGCT
6799	Table 2	NA	65D12	-1	ATCTGCACAGTGTAGCATGGTGACT CCAGTGTCCCTCAAGACTCCATAG
6800	Table 1	NA	68C9	-1	TTAGCATCCACTAGTTACTGCTGG CACTGGGCCACGAAGGGTGACAGGG
6801	Table 1	NA	69F8	-1	GAATCCCGGTCTACCTACCCAAAGTC CCGGTCTCTACCCCTATTCTCTC
6802	Table 1	NA	69H11	-1	TGTAACTTCAAAGTCCCTAACACAT TCGATATTCTCTCTAGCTTCCACT
6803	Table 3A	NA	70B6	-1	ACTCCCACCAAACCCCACTTGTAAT CACTGGTAGTAAAGAGAGATGCAG
6804	Table 3A	Hs.17109	integral membrane protein 2A (ITM2A), mRNA /cds=(139,930)	-1	AAGAGTAAGGCCAACAGATAGAGT GTCCTGGTAATAAGAAGTCAGAGA
6805	Table 2	NA	72D4	-1	GAAAATTGGAAAGGTGATACTTGGGGAC CACAACACGCACATCTGGGAACCTG
6806	Table 3A	Hs.234279	microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA (cds=(64,870))	-1	TCATCTGTGCCATACAGAAATGTCTAC AATCTTCTGCAATACAGGGTCGTT
6807	Table 2	NA	72D8	-1	GGCAAGGGAAACAAACTTGAGTAAATC TAGCTTGAAGGGCTCGGGACCC
6808	Table 1	NA	73C4	-1	ACTCATTTGTCTCCTCATTCTCAAAG TCTTCTGTGGTTGGCTTCAGTG
6809	Table 1	NA	73H4	-1	TCGATGGGCCATTATCCACTCTGCTA TCTCTGAAGAGTAATTTCACCT
6810	Table 2	NA	73A7	-1	AAGGACGGAACACTCACACATCTCTTT AGACAGAAATGTAGTCTACTGCA
6811	Table 3A	Hs.174228	small inducible cytokine subfamily C, member 2 (SCYC2), mRNA (cds=(0,344))	-1	TATAATCCAGTCCATGAGGGTGAA AGTAAATGAGCTGGCTGGCTGG
6812	Table 3A	Hs.3945	CGI-107 protein (LOC51012), mRNA (cds=(84,719))	-1	GCTCTGTTCTGGGGTTGGTCAAAGT CAGGTGGAGTCCAATGTATGAAA
6813	Table 1	NA	75A2	-1	TCCCTGAGATCTAGGAGGGCAGCAT AGTATCATTCTGTATTCCGGTGCCT
6814	Table 3A	Hs.249495	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA (cds=(104,1222))	-1	AGCTGCTACAAAGAAGACATGTTTA GACAAATACTCATGTGTATGGGCA
6815	Table 2	NA	75B12	-1	AGGGATCTGAATACTTGGGTGCAA AATTCTCTGCACTTGTAGATTTC
6816	Table 2	Hs.205442	601439689F1 cDNA, 5' end /clone=IMAGE:3924407 /clone_end=5'	-1	TATGGTTTCCAATATCGACATGGCAT CATTGGTTACATTAGCACTGGGCC
6817	Table 3A	NA	101G7	-1	GGCCTGGGCATAGACTGTGGTGAGG TCACTAGATTATCTGTTCTTCCCC
6818	Table 3A	Hs.179565	minichromosome maintenance deficient (<i>S. cerevisiae</i>) 3 (MCM3), mRNA /cds=(44,2470)	-1	GAGTCCTGATCTCAGCTTCATCACCA ACATTCCTGCCCTCAGTTGAATT
6819	Table 1	Hs.119540	hBKLK for basic kruppel like factor (LOC51274), mRNA /cds=(55,1092)	-1	GGAGGTCTTGGCCACCAATGGGAGA TGAGCCCCAACTTCGATATAGGTG
6820	Table 3A	Hs.215595	guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA /cds=(280,1302)	-1	ACCAAGGGTAAACCTTGAGTGAAATTG TCAGACAGACACACTTTCCACCA
6821	Table 1	NA	105A10	-1	TGCATTTACATTAGCTTCCAATATT ATGGCAGTAACCAACAGTATTATCGT
6822	Table 1	NA	107G11	-1	TTTCCAATGCTCTTGCTCCATTAA ACTTGCTGCTTATAAGAGAA

Table 8

6823	Table 1	NA	107H8	-1	TGTTTCACGATAGAAATAAGGAAGG TCTAGAGCTCTATTCTTGGCCA
6824	Table 3A	Hs.64239	DNA sequence from clone RP5-1174N9 on chromosome 1p34.1-35.3. Contains the gene for a novel protein with IBR domain, a (pseudo?) gene for a novel protein similar to MT1E (metallothionein 1E (functional)), ESTs, STSs, GSSs and two putative CpG Islands /cds=(0,2195)	-1	TTTCATACAAGCCAACAGAACATTCA AGCCACACACTGCACAGGTATGT
6825	Table 1	NA	109H9	-1	AGGAAGCTGTGAGGGTGGGTCATT AGTTGCAGGGATGGTAGTTATGTC
6826	Table 3A	Hs.80261	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related) (HEF1), mRNA /cds=(163,2667)	-1	GAGACAAGCTGGAAGGCCGGACCTC AGACCGGAGGGGGTTATGTCATTC
6827	Table 3A	Hs.1422	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR), mRNA /cds=(147,1738)	-1	ATAACTAGACAAGGTCTGAGCACTT GGGTGGGATGGAGTGAGAAAGGC
6828	Table 3A	Hs.333114	AV713318 cDNA, 5' end /clone=DCAAAC09 /clone_end=5'	-1	ATTAAGTTGGGTAACGCCAGGGTTT CCCAGTCACGACGTTGAAAAACGA
6829	Table 1	NA	129A12	-1	CGCTTCTAGCTGGCCAACAGAGCA GGATTCGTTTCAAGAAAACAAAACA
6830	Table 1	NA	129F10	-1	ATCATGTCTCATTAAACAGAGTGAA TGGAGCAACGTCATCCAGCTTCTG
6831	Table 3A	NA	137D4	-1	TGGTCGCGCCCCAGGTACGGTTTC ATGGTAGGGCTGAATGGAAGATGTG
6832	Table 1	NA	142F9	-1	CAGAAAGATAGGAGTGTCAATGGC AAGGAAACTCAATTAAAGCAATT
6833	Table 3A	Hs.250655	Prothymosin, alpha (gene sequence 28)	-1	TTGCAAACTCTCATGGTTGGGTTGG GTGGTGGAGAGCCGCTGTATCTG
6834	Table 3A	Hs.249495	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA /cds=(104,1222)	-1	TTATTCA CGTCACGATCAGACTGTT ACATTTAGCAATCACAGCATGGG
6835	Table 1	NA	149G2	-1	TGTGTGTATGTGTGTAACCAGGTCTG ACTATAGCTGGCTGTCTGTGTC
6836	Table 1	NA	149A11	-1	AGCATTGGGTTTAGCTTGGTGT CCTAAATTTCAGTGTATTTGCA
6837	Table 3A	NA	151F11	-1	CATAAAC CAGCAGCTAGCGTTCTA TACCAAGCGGTCTCGAGCACAAAGC
6838	Table 1	NA	162E8	-1	TAGTGATAGGCTGGTGGCGGCAA GGTCAGTAATGGGCTTTAACAG
6839	Table 3A	Hs.334330	calmodulin 3 (phosphorylase kinase, delta) (CALM3), mRNA /cds=(123,581)	-1	TACTGTAGAAGAAGAAGAGCACACA TGAGACAGAGAAGGAGGTGGATGC
6840	Table 1	NA	170F7	-1	CGAGGC GCCCCCGCAGGGTACCAAT TTGGATGAATTCTTGATAGATTAA
6841	Table 2	NA	170F9	-1	TTGGGTTCA GAATAGCTTCATCTACT GCCGAGCAAAGTCAATACAGCACT
6842	Table 3A	NA	177A3	-1	GGTAACAGCCATCCCACCAAAATAA TCATCTCATGGCTTTGTCCAGCA
6843	Table 1	NA	331A3	-1	GTATGAATAGATTGCCCCATTCCCTG CCAGCCTGGTAGTGACTTTCCAC
6844	Table 1	NA	331A5	-1	TATAATTCTACCAAAACTAAAGTTTAT TTTGTCGCGCTCCCTGTCCTT
6845	Table 3A	NA	146C3	-1	CTGAAAATTCCTTCGGGTCCATCC TGGCTCTCATCTCCAGTGCTTGA
6846	Table 1	NA	146D8	-1	AGGGTTAACAAAGTATGGAATTCAA TTCTTTTATATGCTGCAGCCATGTC CTG
6847	Table 3A	Hs.153	ribosomal protein L7 (RPL7), mRNA /cds=(10,756)	-1	CCCAATCTGAAGTCAGTAATGAAC AATCTACAAAGCTGGTTATGGCAA
6848	Table 1	NA	158G6	-1	CCGAGGTACTCTCTTAGAGAAAGGT ATTGGATGCTCGGGTTGCTGTAA
6849	Table 1	NA	158H6	-1	GGGGGTTGGAAAATAGTCGAGAATTG ACAGTCCTCTCGAAGATGCTTTT
6850	Table 3A	Hs.119598	ribosomal protein L3 (RPL3), mRNA /cds=(8,1217)	-1	TTGAGACCCCACCAACTGCAAATCT GTTCTGGCATTAAAGCTCTTCTT
6851	Table 1	NA	158G11	-1	AATGAAAATCTCAGCTCTCAGCTCA CAAATCTGAATTAGGTGTCTT
6852	Table 3A	Hs.326249	ribosomal protein L22 (RPL22), mRNA /cds=(51,437)	-1	TCGTCTGGTTATCGGAAGTAACG TAATTCGTAACTCTCTTGCTGT
6853	Table 3A	Hs.297753	vimentin (VIM), mRNA /cds=(122,1522)	-1	TCGGTTGTTAAGAAACTAGAGCTTATT CCTATCCAAACTCATCTTGCCT
6854	Table 3A	NA	155H10	-1	AGATAAGAACCTCATCTAAAGCATC CGGGCCTGGCATCTTGTCATGC
6855	Table 3A	Hs.108124	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	-1	ACTGATTTCATCAAGTTGACACTGG TAACCTGTGATGGTGACTGGAGG
6856	Table 1	NA	159F6	-1	AATCATGGCTACCTCCCTCCCTTT ACAGTCACAAGTCAGATGTTGG

Table 8

6857	Table 3A	NA	166F3	-1	AATAAAATCCCATAACCTCCCATTGAAC TACCACCCACCCGACCACCATAA
6858	Table 1	NA	166F6	-1	CAAGACATTTCCAGCCAACTTCAAGAA TGTAGATCTTGAGCCAGACAGCT
6859	Table 1	Hs.8121	Notch (Drosophila) homolog 2 (NOTCH2), mRNA /cds=(12,7427)	-1	GAGGTACTGGCCTGTGAAGCCCTGA AGGCACTGGCACTGGTAGGAACCAG
6860	Table 2	Hs.25130	cDNA FLJ14923 fis, clone PLACE1008244, weakly similar to VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1 /cds=UNKNOWN	-1	ATCTTCTGTCAGTCAGTCGCTGCT CCAAGATTGAAACAGTCTGTGTC
6861	Table 1	NA	168A9	-1	TGGATGGATTCCAAGTGGCCCTCATA TTTATCATGGTCTTAAATAGCA
6862	Table 1	NA	171F11	-1	TTCACTTAAAGGAAAGAGAGATACAT TTTAGATTATAGAGCATCGCCTGC
6863	Table 3A	NA	171G11	-1	ATCTTCTATGTGCGCCAGATAATGA TCAAGTTCACAGGTGGTCTTACTT
6864	Table 1	NA	175D1	-1	AGTTCTTAAGTCAAATGACACATTAG CCCAACGCAATCCCAGCCCCAGC
6865	Table 1	NA	182H1	-1	CCCTCTCTGACATGAATTAGGCATA ATTTAGCAATCGGTTCTCCCAA
6866	Table 3A	NA	184B5	-1	ATACAGTGAACTGGCCACTGGCTGTT TGCTATATAAATGGTATACTGCTT
6867	Table 3A	NA	184D2	-1	AGGTTACTAAAAGCATCATTGGCGT GGTCCTCTCACTACCAAAAGGGCAG
6868	Table 1	NA	184H1	-1	CTGGGTCAGCAAAGAGGGTAGCA AGTGTGCCCTAGAGATGAAAGAAATG
6869	Table 1	NA	46D1	-1	TTTAGAGTACTTAGAGGAGGACAGG AACACTGAGACAGACACGCAGGC.
6870	Table 1	NA	98C1	-1	TGTTGAAAACACTACCTTCATGGGAGC AATGACAAGCACATGTCAGGATT
6871	Table 1	NA	98C3	-1	TTTGCCCAAGGTTGGGATTGGTC TTCTAGAGCTCTCTCACTGGCTTG
6872	Table 2	Hs.205442	601439689F1 cDNA, 5' end /clone=IMAGE:3924407 /clone_end=5'	-1	TTTTGACGCTCTCACTGGCTTG GCATTTGATGTTCTGTTGAAGCC
6873	Table 1	NA	98H4	-1	CCTATAATGGGGAAAGATGCTGGTT AGATGTTTATTTAGTGGGCTTGC
6874	Table 1	Hs.169363	GLE1 (yeast homolog)-like, RNA export mediator (GLE1L), mRNA /cds=(87,2068)	-1	CCACAAACACACCTGCCAACAGACA TTAGCACAGAGGAACAGATCCAT
6875	Table 3A	NA	113F12	-1	GACACCACAACTCACCTCCTCTATT TTAGAGATCCGAGAGACATTACGGC
6876	Table 1	Hs.30212	thyroid receptor interacting protein 15 (TRIP15), mRNA /cds=(15,1346)	-1	TGTTACAATTCAGCAGTGTGAATTCA GTGAACACTGGTTGAGGAGTGCCT
6877	Table 3A	NA	173A10	-1	CCTCCGTATTCTCCAAGTATTAC AAGCCCTCCCTAAACCCCTCT
6878	Table 3A	Hs.334853	hypothetical protein FLJ23544 (FLJ23544), mRNA /cds=(125,517)	-1	ACAGCCCATCTGGGATGAGCCGCTTT CAGCACCAGTGTCTCAATTCT
6879	Table 3A	Hs.20252	DNA sequence from clone RP4- 646B12 on chromosome 1q42.11-42.3. Contains an FTH1 (ferritin, heavy polypeptide 1) (FTH1.6) pseudogene, the gene for a novel Ras family protein, ESTs, STSs, GSSs and a putative CpG island /cds=(0,776)	-1	TAACTGAATACAGTCTCATCTTGC CGCCTGGCTTACCTATGTGAA
6880	Table 1	NA	174D1	-1	AGGTACTACACAAGGTGTCAAGATGG GGTTGCCACAATGACTAGGACAAAGA
6881	Table 1	NA	45B9	-1	CCAAGAAGACAGAAGGAAGTGTGCGA ACACCATGACAAGAGCTTGCAGAA
6882	Table 1	NA	45H8	-1	GAGAGCTTCTCCCGCCTCAGTT CTGATGGATCTAGCCATGTTGAAA
6883	Table 1	NA	111H6	-1	TAAAATTTCTGCCAGGTTCCAGAG AAAGAGTAATTTCTTGTAGTAC
6884	Table 1	NA	111E12	-1	CGCTCGCCGGGCCAGGTACCAAAAC TTTCATAATAAAAGGTAGGAAGGAT
6885	Table 1	NA	111H11	-1	TGACTTCACTGAAGGCTCATCACCC AAAGTAGATGTTAAAACCTTAAT
6886	Table 1	NA	112H3	-1	TTTATGTGGAAGGCTTCCCTATTAC TCCCAAGCGAAATTCTGTAGTCTTC
6887	Table 1	NA	112E9	-1	TAAAATGTTGCCAGTGGAGGACCGAA TCAAGGTTATTGCTGACCTCATTT
6888	Table 1	NA	114G3	-1	AGATATGTTCTGAGCCCCGCCACAC ACTGCTCTGGTTACAGGGAGAGAAG
6889	Table 1	NA	117H6	-1	GAGGTTCTTCACTCCAGAAGAAGCA ACAGGATTCCAGATCAGGGCAAC
6890	Table 1	NA	165E7	-1	CTGGTCTGTGCTGGCTTATGAC AGGAAGTGCCTGTGGGTTATCTTA

Table 8

6891	Table 1	NA	165E11	-1	CCCAACGCTTGTGCGTATGTATGT GTGTATTAACATCCTGTCCCCAT
6892	Table 1	NA	165F7	-1	GCATAAAGGCAGCCATTCCATTCTC TACATTCTCTAGTGATAGCAGAGG
6893	Table 1	NA	176A6	-1	CGTTACGCAATGGAGAAAGTCCCCTG AGGCTGAATAATCACATCTGTATC
6894	Table 1	NA	176G2	-1	AGGCCAAATCACCGCACAGTTGAATT GCTGATTCTAATTGGTAACAATAA
6895	Table 1	NA	176E10	-1	TTTAGTGTAAATTGTGTGATACGCAA ACCTTAGTTAACCAAGTGATGA
6896	Table 3A	NA	176F11	-1	CCTTGTGCGTGGGTATATGCATGA TCTTACCTTGTGTTGACTATGAA
6897	Table 1	Hs.232400	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(169,1230)	-1	AAATGATATGTTAACCAACCCAAATCTT CACATGGGGGAAGGGGGGG
6898	Table 1	NA	71F2	-1	GGCCAAGCTTTATTATGAGATCT TTGAGTGAATCAGCATGTCCTC
6899	Table 1	Hs.172028	a disintegrin and metalloproteinase domain 10 (ADAM10), mRNA /cds=(469,2715)	-1	TTAACAGCATTGAAGGTGAAACAGCA CAATGTCCCATCCAAATTATTT
6900	Table 1	Hs.180610	splicing factor proline/glutamine rich (polypyrimidine tract-binding protein- associated) (SFPQ), mRNA /cds=(85,2208)	-1	AGGTACGAAAATACATTCTGGCATCA CACCCCTGAACCCAAGACTGTTCT
6901	Table 1	NA	124G4	-1	GAACACTACTGGCAGTTGGTTCA GGGAGATGGGATTGACTTCGCCT
6902	Table 1	NA	124C8	-1	AGAGCTAATATACAGAGTACCTGACA CACTACCTCACCAACAGTTAAC
6903	Table 1	NA	124F9	-1	GCCCCAGGCAACAAAGAATACTTTTATC TTTGATCCGTTCTGTTTATCCAGT
6904	Table 3A	NA	127A12	-1	CTGAGGGTAGACTGTGGCAAAGAG GACAACCTCCCTCCCTAAAGGGAC
6905	Table 1	Hs.50180	601652275F1 cDNA, 5' end /clone=IMAGE:3935610 /clone_end=5'	-1	TGCCCCAGACCTATTTCCTTAGGACAG TATTCTAAAGTCAGTAGTCCAGT
6906	Table 1	NA	161E8	-1	GCCCTGTCCCTTGAGAGGCTCACAG CGATGGAGGCCACTTTGTTGTTG
6907	Table 1	NA	186E8	-1	ACCAAAAGGGCTACATTACCACCAAC TGTATCATAAAAGCCAGCCACCTT
6908	Table 2	NA	191F6	-1	AGCTGACGATTTCTATCCGGGCCTA TAGTGCATGTATGGCAATTGAGCA
6909	Table 3A	NA	193G3	-1	CCCCAAAAACAAACAAATAAACACACA CCAGATATCAGTCACATCCTTGA
6910	Table 1	NA	194C2	-1	AGCTGTATTGCTGATTTGTCCC CACCTGTTCAAATTCCAAAGCT
6911	db mining	NA	458C6	-1	CTCACAGCGAACGCTCTGATCCTTGT TTCTCAGGAAACACTCAGGAAGTG
6912	Table 1	NA	458E4	-1	AGAGAAAATGAGAGACAGACAGTG GTGGGAAAGTCAGCGAAAAGGAAAA
6913	Table 1	NA	458G10	-1	TCCCTGAGTTATACACCGTGTATG AGTGATGACAGCCATTCCCATGC
6914	Table 1	NA	459B3	-1	TCGCTTCAGGGGTCAAGCCAAAGATA GACAGCCAGGTAACTTGAGTGAC
6915	Table 1	NA	459D2	-1	GGACAGTACCAAACACTCCCTCCTC CCCTCTGCTCTTTGCTTACTTAG
6916	Table 1	NA	459E6	-1	GACCAAATACTGAACCTCCACCCCTGC ATAATAATCATGAACACCCGACCA
6917	Table 3A	Hs.20830	DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein In an intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the homolog of the rat synaptic ras GTPase- activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS /cds=(163,2184)	-1	AGGTGAGCAGTGCTCTGACATACTTG CAAACCTTCTGCACAAATGTGCT
6918	Table 3A	NA	460D5	-1	CAGATCCAATGAGGGTCCCATCTCTT CCCACTTCATCCCGTGTGTTCT

Table 8

6919	Table 1	NA	460B9	-1	CCAACCAAACCATCAAAACAGCAGGGAGCTAGTGAAGAGGTCTATTGTTCC
6920	Table 3A	NA	461A4	-1	ACATCGCCTAAAACCCTGCATCGTAAACATTACCTCAAAGTCATCTCT
6921	Table 1	NA	461G6	-1	TTTTCACTCCTCAGAGTCTACTCCACCTCTCCTACTCCCCAGGACAC
6922	Table 1	NA	461D9	-1	AGATCTGTGTTGTCAGGTATAAGAACACAATCCAGACATGATCT
6923	Table 3A	Hs.80768	chloride channel 7 (CLCN7), mRNA /cds=(38,2455)	-1	TTCATGAACCTGGAGAGGTCCATGGTGCACACTCCGCTCGTCTGGGACAC
6924	Table 1	NA	461H7	-1	CTGGCAATATTAACTGGGTTGTTCACTCTGGCTATAAGCCATAACAGG
6925	Table 1	Hs.333513	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating) (SCYE1), mRNA /cds=(49,987)	-1	TGCCATTCTTTGTTGAACCTGTAAAGGCCAGATTCTGAAACCT
6926	Table 1	NA	463A5	-1	TAAAGCACTTATGAGAATGCTGCATTGTACATGAGCTACGCCATCTT
6927	Table 1	NA	463B2	-1	GCACCCACCTCCTCAGTCAGACAAGCCCAGCCCCAAATACCAACTATCT
6928	Table 1	NA	463C5	-1	AGCGCATGAGTGACTCCCATCTATATATGTCAGTCGTCCTGTCAGG
6929	Table 3A	Hs.40919	hypothetical protein FLJ14511 (FLJ14511), mRNA /cds=(22,1272)	-1	GAAACAGTGGCCGGGTGCTAGTGCCTGTCCAGATCTCACCTACACC
6930	Table 1	NA	463H5	-1	AGTCATTACACTGATGATAAACGATAGTAGCTTCAGGTTGCTTCT
6931	Table 1	NA	463A7	-1	GCTTCAAAATTCTTACCCCCAACCTCTGGCACCCCCAAATTGTATCACTA
6932	Table 1	NA	463B10	-1	GAGGAAGGGCTGGCTTACTCCCCACAAAGAGGTGTTCTTAGGCCACAC
6933	Table 1	NA	463C7	-1	CCAACTCTAACTTAAACCCCTCATACAGGACATAAGCTTGCAGCCGCATCT
6934	Table 1	NA	463F10	-1	TGCTCAATGTGCACTGATTTTTATTCAATGTTGAAGGGCGTTATGA
6935	Table 1	NA	464C2	-1	TGCTAACACAGCTTCGGTATGTTAATATTCTGTAACCTCTTCTCA
6936	Table 1	NA	464C5	-1	GGAGGAATGGCTGTGCCCCGTCCTCCACTTAAGCGACCTGAGTCAGCAG
6937	Table 1	NA	464C10	-1	ACACACACTTAAAGAGTACAGATGAGAGCAAAAATAAGTGGCAGGTCTT
6938	Table 1	NA	464D8	-1	TTTGTGACTGTGCACTGTTGAAAGAATAAGTTCAGCTGTCT
6939	Table 1	Hs.221695	7k30d01.x1 cDNA, 3' end /clone=IMAGE:3476785 /clone_end=3'	-1	CTTGTCTGTGGCTGGCACACAGTGGTCGGTTGTGTTGAATG
6940	Table 1	NA	464E7	-1	GAATTCTGAATACATGTTGACTGTGTTCTTGACCTGTGTTCTTAGG
6941	Table 1	NA	464H12	-1	TGAGTCCTGGCCTCAGCTCTAATCCTAACCTAAATAGATTGCGTTT
6942	Table 2	NA	465B3	-1	TCTTCTCGTCTTGTCTATTAAATTCTACACGGGACATGCTTCATGTT
6943	Table 1	NA	465G2	-1	CCAGAGACTCTAAAGCAGAATCAAGGATGCTGAGTCAGCTTACCTGTC
6944	Table 1	NA	465H5	-1	CCCATAAAAGAGGAATAAGCTACTGTCAGTCAGCTTACAGGCTT
6945	Table 1	NA	465A12	-1	AGAGTTGTAACACAATCCAGTCCACATGCTTACATCCAAATGGCAATGATGAT
6946	Table 1	NA	465F7	-1	AGCTCAAATATGGCAAAAGTGTGCTTACAGCTTACATCCAAATGGCAATGATGAT
6947	Table 1	NA	465G8	-1	TGGGTCTGCTTTCACATGAAAGTGTGCTTACAGCTTACATCCAAATGGCAATGATGAT
6948	Table 1	NA	465H10	-1	GGATGAGGCCACTCACAGCAGCAGCAAAATGGCAATGATGCTTACATCCAAATGGCAATGATGAT
6949	Table 3A	Hs.136309	DNA sequence from clone RP4-612B15 on chromosome 1p22.2-31.1. Contains the (possibly pseudo) gene for a novel protein similar to 60S ribosomal protein L17 (RPL17), the gene for CGI-61, endophilin B1 and KIAA0491, ESTs, STSs, GSSs and two CpG islands /cds=(1011,1406)	-1	AACCCAAATCCAAATGCGAGGATAGAGAATTGTTATGAGAAACTGGAA
6950	Table 1	NA	515C12	-1	CGCTTTTGATCTGATTACTATTTCACACAGGTTACAGCTATGACCATGA
6951	Table 1	NA	515H10	-1	CTGCCGCTAATTCACTGATGAAATTTCGATCGTCGCCCTCCAGGTACATAT
6952	Table 1	NA	55G3	-1	AGGCCTGCTATTAAATTATCCCATACCTCCCTACAGAAATTACACTCGCA
6953	Table 1	NA	55F9	-1	GGGAGAAGTCTTAAACTAAGGGTACAAATGAATTGATGCTGGGGC
6954	Table 3A	NA	99E7	-1	ATTACGCTGTTCCGGCCCGAGGTACACAAACACTTCAGAAAGCAAAGTT

Table 8

6955	Table 1	Hs.319825	103C4	-1	AAGATATGAAATATGCCCTACCCGAG AGCTTGGCACAAAGTGGAGTCAT
6956	Table 1	Hs.17481	mRNA; cDNA DKFZp434G2415 (from clone DKFZp434G2415) /cds=UNKNOWN	-1	GTACAGAGATCGGATCACACAAGCC CGGAGACAGTCAGCTTCTCACTG
6957	Table 1	NA	116C9	-1	AATGCACTTGTGATAAAGTGACAGCA GGGTTAGACATTACTTCAAAGCT
6958	Table 1	NA	128F5	-1	CCACTGCTCAGGAAACTGCCCTGTTCG GTGCTCTCCAATTCAATTAAAGCT
6959	Table 1	NA	135F10	-1	AGTGCTGGATAACTGCAGAAAGAGA TAGAGAAGAGAGATCAGTGAGAGC
6960	Table 1	NA	189F3	-1	AAAGTCAGGACCTTGCACTTGCCCG CCTCTGCCCTCACAGCTTCTCA
6961	Table 1	NA	189A8	-1	TAATCAGGGAAGAGCTTGAGATCATT AGCAACTGAACGTGAAACAGGGAGTT
6962	Table 1	NA	195H12	-1	CTGGGTACGTCGCCACCAATGGT ATCTGTGTGTTAGGCATTAGGCTG
6963	Table 1	Hs.292457	Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds /cds=(498,635)	-1	GGTGGTAGGTAGGTGGTATTGGGG GCTAGTATCCGAGCAAAGATGGTG
6964	Table 3A	NA	466C4	-1	CAGCCCTGCTATCTGGTTGTTCAT- GTACTCTGTAAGGTGGAGACCT
6965	Table 1	NA	466D1	-1	GAAGGTGAGAAACCCGAGAGACACC AACTATGATTTTACTTTCTGTT
6966	Table 1	NA	466G2	-1	ACCAACCCCTCCCTCCCTCTTAAAC TCATCTCGAACATCTCTCATACAT
6967	Table 1	NA	466H5	-1	CTCTTATCCTGCTCTGCCCTGAAACT TGAACCCCCAGTGCCAATCTCATG
6968	Table 1	NA	466B7	-1	CGACCTAACTCTGTCCCCAGAAGGC AGACCAAGGACTCCAGCCCCAGGAG
6969	Table 2	NA	466B10	-1	GCCAAATCTTGTCCCTGTACAAAGTA CAGATGTTTGACTGAAGTTCCA
6970	Table 1	NA	466C9	-1	GCCACAGTGAATAAATACAAGGCAAG GCTCATAGGTAACAAAGTTCTAT
6971	Table 1	Hs.7187	mRNA for KIAA1757 protein, partial cds /cds=(347,4576)	-1	AGTGGAGTGTACACCTGCTGTAAC CTTGAACCTTCAAAAGAGATGT
6972	Table 1	NA	121F1	-1	AAACCCACCCATCATTCGCTGACT ACCCATCTCCGATTAACTCACC
6973	Table 1	NA	121A11	-1	AGGGAACAGAGCCAGGATTTAAACTC TAACAAATTGCTCCACAATTGCA
6974	Table 3A	NA	121F8	-1	CTCCTGGCACGACAGAAACTAGTAGTT TCCATGCTTGAAGGACATAGGTC
6975	Table 1	NA	178B2	-1	TGAAACCTGTTCCAGGTATGCTGATA GATGTCGGTAGGGCATCTTAAATT
6976	Table 3A	NA	178B5	-1	GAGGTACTATAAACCAGATGCCAAA ACACCTGCCCCCTGGGTTGGCG
6977	Table 1	NA	178F5	-1	ACATTCACTGTTCCACTGAGGTCT GAGTCTTCAAGTTTCACCCCAGC
6978	Table 1	NA	178C12	-1	TTAGCCCTTCTGGCTAATTAGAAT TCAAGCGTCACAGAGCTGGGG
6979	Table 1	NA	462A11	-1	TTCAACCGAGGTGAACAGTGTGATGT CTGTGGGGAAAACACGTAGTCAGG
6980	Table 1	Hs.13231	od15d12.s1 cDNA /clone=IMAGE:1368023	-1	GGAAAAAAAGAAAATTCTGAGATTC CAGTGTATACAGAAAGTGTCTTCCAT
6981	Table 1	NA	462D9	-1	GAGTTACGTGGGTGGCCCTCCTC AGTGTCTTAGGGTACTGTACTGTC
6982	Table 1	NA	462E8	-1	CCACCTTCGAGGTCCCTTCCGGCTA AGATGCCTGAAATCTCAAGGAAA
6983	Table 1	NA	462F9	-1	ACAAGGCAAAGCTTAAAGAAAACACTA AACGAATGAGTGAAGAAGCGGAG
6984	Table 1	NA	462F11	-1	TTCTCAATAACAAACCCAGGGCTTTC ATAATGCATGATCAAAATGTGGA
6985	Table 1	NA	462G12	-1	ACAGAAAATAGGGTGTATATCAGCAT. TACGCTGATTCAGCAGAAAGATAGC
6986	Table 1	NA	462H9	-1	TCTCGACTGACACCCACTATAAATT CCTGGGTTGAAAAACTTTCTTT
6987	Table 1	NA	472B1	-1	TCCAAACCCCTCATTACAATCTAAC ACACTTCCCCATCATGCTCT
6988	Table 1	NA	472C1	-1	GCATTATTCTTCTACAGAGAACCT GGCGCTGGGTCTGGGAAAGAGC
6989	Table 1	NA	472E6	-1	ACCCACAATTAGTGAGAGTGCCTTG AGCTTGAGATTCCTTACCTCCCT
6990	Table 1	NA	472F4	-1	TGGATATAAAGTGTGTGTTCTGACAG AAAATGGGGAGAGGTGGCTATT
6991	Table 1	NA	472G2	-1	GCCAGAAAATCTGGTTCCCTGGT TCCCTCCAATCTCTTACCAA
6992	Table 1	NA	472D7	-1	CCATTGTCGCCGGAGCTGGAAAGA TAGTTAGAGAATGCCTTACGACTT
6993	Table 1	NA	472G12	-1	CAGCACCCAGTACAGGTATGCAGGA AGGACTCGCTGACTTAGAGAGTGG

Table 8

6994	Table 1	Hs.75354	mRNA for KIAA0219 gene, partial cds /cds=(0,7239)	-1	AACACACCAGAAGGAAAAGACACAGA CAGGGAAATGAAGCCTGCAAAGTCC
6995	Table 2	NA	64G9	-1	GTAACTCAGTCCCCCAAAGATTCAT AGTCAGCAGGATTGGCCAGCAAT
6996	Table 1	NA	467E5	-1	CGCCCAAATAAAATCTCAATACC AGTTCTTCCCCAGTACCCAG
6997	Table 1	NA	467A8	-1	AGTCACAGGATTTCTCTGCACCTCA TCTGCAACTCTGAGGCCCTACTCAA
6998	Table 1	NA	467C9	-1	GTAGAGCCCTGGTGCCTGCTT CAGCTACCATTTCTCTGTGACC
6999	Table 3A	NA	467F8	-1	CCACACAAACACACACACAAAAAGT CAACCCACACGAATATACCGGAAA
7000	Table 1	NA	468E6	-1	CAGTTGGGCTGTTAGTAGTCTGTAC ACAGGTGAGGAGGAGCAAGAGATCC
7001	Table 1	NA	468B9	-1	AATCTATTATCAGGCAATTAACTACTG AGCACTCTCTGCCCACACTGT
7002	Table 1	NA	468E10	-1	AGAGGAGTGACGGTGAATGGTACTG AAAGCGGTTGTAATTGCGAGAGAG
7003	Table 1	NA	468F10	-1	TCTCTTGTCTGATTCTCTCCCATC TACAACAACTCCACTCCCCAAAG
7004	Table 1	NA	468F11	-1	CACCTAACCAAGCGGGTTGGCTGA TGACCGATGACCGTAAGCAGTAAGG
7005	Table 1	NA	468G12	-1	ACCTCTTCTTAGCAACACTAACAC TCCACACTGGGAAATTATACTCT
7006	Table 1	NA	468H11	-1	ACTACCGCACACAGAACACATGACC AGGTGAGTGCAGACACGACATCAG
7007	Table 1	NA	469B6	-1	CAGTTTTACTCTGGTCATCTCTGT GAGTGTGGATTCTCTGCTGCCCT
7008	Table 1	NA	469D2	-1	TTTATTTGGCTGAAGTTGGGTATG GCTGCTTGTGGCCTCTGCTGGG
7009	Table 1	NA	469A10	-1	ACAGCTTATAAGCACTTTCTCATGC ACTTCTCTCGCGTATTGCAAA
7010	Table 1	NA	469E12	-1	GGGGCTAAACCTGTGACTTACTGCT AACTAACATCAAAGGAAAAGCTGG
7011	Table 1	NA	469F8	-1	ATGATCATTGATAGATAATTCTAAGAG CATCAGGAATGAGGATGCGTGC
7012	Table 1	NA	469G8	-1	GACAACAAACCTGCTTGTGTTGTTAC CCACAGCCCACGTAGTATAAGAAGT
7013	Table 1	NA	470B2	-1	TCTCAATTATTATGCTCTAAGGCA GTGTCTGCTTCCCACCATCCGC
7014	Table 1	Hs.118174	tetratricopeptide repeat domain 3 (TTC3), mRNA /cds=(2082,7460)	-1	TGAGTATTTAAATCCCCTGTTGG ATGCTTCCAGCTAAATAGTCTACCT
7015	Table 1	NA	470C3	-1	TGGTTTACTCAGATCTTCCCTCTT AAGTGAGAGTTAACTACATTTC
7016	Table 1	NA	470D5	-1	GTCAGAGCTAGAAGAACCAAGTCTT CCTTCTTCTTCTTCTTCTTCTT
7017	Table 1	NA	470E1	-1	CTTCTCTTAGGATCTGGAGGGAGGG GAGTGTAGAGCTTGTGACCCATG
7018	Table 1	NA	470E5	-1	CTGAACCGAACAGTTCTTGGACTA CCAGTTCTGAAGTGAAGCTCAGA
7019	Table 1	NA	470F3	-1	AACAAAAGCACTGACAAGCTCATATG AACAGGCTAAAAGTGAAGTGAAGT
7020	Table 1	NA	470G6	-1	TTCTCTTCTATATCTAGCTAAATTGC CTGTGCGCTCCCATCTCTCTCA
7021	Table 1	NA	470B8	-1	ACACACTTGATAAATTAGACCGATGC AAACCGCAAGAACCTCAAATCAGCT
7022	Table 1	NA	470G10	-1	ATAGTAGGTGAGCCAGTAGTGTGAAT GCTTGTCAAGCTTCAAGGATGTTGA
7023	Table 1	NA	471D8	-1	AACCACCACCCAGCTTCTGGTACAA GCAGGGACTCTGGCTACAGTGCTA
7024	Table 1	NA	471F1	-1	TTCTCCCCCTCCCTCCCAATCCAC AAAACACGTAATTCTGACTATCCA
7025	Table 1	NA	471F4	-1	CAACATTCAACAAACTGGTCCCGAA TTAGTGTAGAAGGATCCTCCTCT
7026	Table 1	NA	471F6	-1	GAGAGATTATAGCACAGTCTCCAGG GCTCAGTCAGGTCTCCAGCAA
7027	Table 1	NA	471E9	-1	TTCAATGCTTGTCTCCCTCCCTCGAG ATGTTTAGAACAGATCCTCCTCT
7028	Table 1	NA	471E11	-1	TCCCTCTCTAGGGCTGGGAAAGAAA GTTCACTTCACTCAGATGCAAG
7029	Table 1	NA	471H11	-1	TTCTGTTGGCTGCCAGCTCATCCAT TCATCCATCACCTGCCAGCTAGAC
7030	Table 1	NA	473E4	-1	ACACAGTTTGCTCCCTTATTTC CCGTACTCGAAACATTTCATGCA
7031	Table 1	NA	473F3	-1	ACCAAATCGAAAAATACAGAATGCC TGAAATTGAGTCACACCTAAAAA
7032	Table 1	NA	473E11	-1	GAGTCCATAAAATCTGCATTTCATGTA GTGTAAGACTTCTCCCAAAGGT
7033	Table 1	NA	476C1	-1	TCATTTGAGTTCTTCCCATCTCTC ACAGTTGATTGTTCTGTCCCTTC

Table 8

7034	Table 1	NA	476D3	-1	AAAATTCA G C C C T C C T G G A T T C A C G T G C C A A T G A A A G T C C C C A A A C T A G
7035	Table 1	NA	476F5	-1	T T T A A C A G G A A A G G C C C A A A T T T T T T A T G C T G T C T A C A A T C T G G G C C
7036	Table 1	NA	476G3	-1	A G T T G C A T G G T T G T C T G G C T G C G G T G C T T C T C A C A C A A G A A G C C C A G
7037	Table 2	NA	476G4	-1	T T T C C T T T C C C T T G T C C C T T G G C T T C C C C C A T C A C C G A A T C C C C C T T C
7038	Table 1	NA	476A10	-1	C T C C C A G C C T G G C C T G A G T C C A G A G C T T C T C T T T C A T G G T T G G G T T
7039	Table 1	NA	476G8	-1	G C C A G T G T A C G T T G C C A G G C A T T C A T G T A A G G A A A A C T C C A A A T A G C C A
7040	Table 1	NA	476H10	-1	C C G T C T C T T T G G G T G T T C C T C C T A G T T C C G C G G A A T C A G A G T T C A
7041	Table 2	NA	477E1	-1	A T G A A C C C T C A C C T G C T C T G C A G T G C A G T T T G A T T T A G T C C C A G C C A A A
7042	Table 1	NA	477E6	-1	A G A T A G A T G G T A A A A T G T G A T G C A A T G A A A A A A T G G T A A T A C A C A C A C T C T C C A
7043	Table 2	NA	477A11	-1	T G A G T G G G C T T C T T A T G G T A C A G T C T C T C T C T A T G A G G G G C T T C A A A
7044	Table 1	NA	477D9	-1	T G G G C T T C C A A A T G G T A C A A T G G A G T A A T C A A G C T C A T G G A C T G A G A G T T
7045	Table 1	NA	477D10	-1	C T T G A A G C T A C T T G T C C C T T C T G T G C C A G A C C A C T T A A T G G C T A C C C A C
7046	Table 2	NA	480A3	-1	T T C C C A G G G C G C T C A T C T A C A G C C T T A C T G T G A C T C C A C T C A G C A C C A G
7047	Table 1	NA	480B5	-1	A T T C C C C T A A G G T C C T G T C C C C C G C C A T G C A C G A C T G G T C A C A T C A A A A
7048	Table 1	NA	480D2	-1	A A G A C A C C C C T C T G T T T A A T A A A A A G T T G T C C C T C G A C A T G C A T A A T
7049	Table 1	NA	480E2	-1	C C T G G T T A C A A T A A T G A A A C T G T C G T G G A G T A A A G G G G A A C A T G A C C A
7050	Table 1	NA	480E3	-1	A G A A C C C C A C A C T C G G G A G A C A A T A A A C T G C C A T T C A T A T A A C C A A C A G A A A
7051	Table 1	NA	480F3	-1	C G C C A C T G C T T A A A G G A T T C A G A C A A A T T C C C A G G T A A A G T T G C C A G G A C T
7052	Table 1	NA	480G4	-1	A C A A T G A T G T T G A A A C G C A C T C T G A A T C T G T G A A A G C T A G A T A A G T C C T
7053	Table 1	NA	480C8	-1	G C C T T C C T C C T C C C C T C T G G G C C T A T G T C C T A G A T A A G C C T G T T A A A
7054	Table 1	NA	480D9	-1	T G T C A A G A T G A C A G A T C T T A A T C C A G A G T G G A G G C T G T T C G G C C T G G A G
7055	Table 1	NA	480E7	-1	T T T A T G T T T C A G C C T C T T C T C T C C C G T T G A G T C T G C C A C A A G T C C T G C
7056	Table 1	NA	480E11	-1	A T T G T C C A G G T G A C T T G A C A C T T G C C T A C C G G A A A G T T G G A T G T T C T T
7057	Table 1	NA	480F8	-1	T A A A A T A T G C C C T A A T T T A A A G G G C G C A G G G T C C C A C A A C A G G C C A C A G A
7058	Table 1	NA	487F11	-1	A A A T C T C T C T C A C G T T C T G T T T G C A T T T A A T C A C C A G G T T T T A G C G C
7059	Table 3A	NA	499G1	-1	G C T A C T G A T G G G T G G C C C T T T A T T C T T G T C T T T A T T G T T G T G C G A G G A
7060	Table 1	NA	518F10	-1	A A A A A T T G G T A G C T G C C C C C A T G T G G T A T G A T G T T A A T T G A A C A A C A T
7061	Table 3A	NA	524A12	-1	A C C C G G C A C G T C C C T C A A C C C C T T A A T T C T T C C A G C T T T C A T A T T A
7062	Table 1	NA	526B9	-1	C T C A A G A G G G C A T A G A C A T T C C A C A C G A G G A C T G C A T T C G T C A G G G T A A C
7063	Table 1	NA	583B5	-1	A A C A A A T C C C A A T T A A C T G T A T T C C C C T T T C C C C T A T G A C T G C T G G G T
7064	Table 1	NA	583D6	-1	C C G T T G T C C G A A A G C T G C T T C C A A C T A A G G A C C A G A G A T G G G A G G G A G T
7065	Table 1	NA	583G8	-1	T T I A G C C C C A A A G A A G A C T T T C G C A T A A A T T C T G C C G T A A C C C T T G T T G G A
7066	Table 3A	NA	584A1	-1	C A A G C A G C C A A A T A C A G A G G C A C A C A A C A A T C T T G G C C T G A G C C A G A A C A A
7067	Table 1	NA	584D3	-1	A T A T G A A G A T G G A T T G G A T G A G G A C T G A C A A A A C G A A G A C A T G C C G G G C C
7068	Table 3A	NA	DNA sequence from clone RP4-620E11 on chromosome 20q11.2-12 Contains t		-1 A T G C C T A G T C A G T C A G T A T T T C T C T T G C T G C A G G T G T C T A A A A A C C C A C
7069	Table 3A	NA	591H9	-1	C C T T C G C A T T C C C C C A T C C A T G C T C C A A G A T A A T A G A T T T T C T T T A A A A

Table 8

7070	Table 3A	Hs.6179	DNA sequence from clone RP3-434P1 on chromosome 22 Contains the KCNJ4 gene for inwardly rectifying potassium channel J4 (hippocampal inward rectifier, HIR, HRK1, HIRK2, KIR2.3), the KDELR3 gene for KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3, the DDX17 gene for DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD), ESTs, STSs, GSSs and six putative CpG islands /cds=(307,2259)	-1	GGGGAAACACTTGGTTGAAAGCACA GAGCAGTTGCCATGTTCTCTG
7071	Table 1	Hs.44577	602388170F1 cDNA, 5' end /clone=IMAGE:4517129 /clone_end=5'	-1	ACTGAATGGTCGAAATCACATATGCA CCACACATACTGATCTTAAGTAAC
7072	Table 3A	Hs.108124	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	-1	CGAGGTACAGCAAAGCGACCCCTGG TGTCTAGATCAGACGGAAATTCTC
7073	Table 1	NA	119F12	-1	TACAGAAGAGCAGAGACCAACCTCT CAAAGTTGGTAGTATTAAACCCAG
7074	Table 1	NA	119G10	-1	CCAGATTGGCTGATGTGTTAGTAGT TGTGGCACACTCACCTGTCTTCC
7075	Table 1	NA	485A6	-1	CTTTCAGGTTTCCCTTCCGCCAT TGTTCCTCCGCTCGCTAACAGTGAC
7076	Table 1	NA	485D5	-1	TTGAAACATTGCGAAAGTAACATCTCT CACTCCCAACACCCACAGCTTATCG
7077	Table 1	NA	489H9	-1	AGTAACCAACCAAGCATAGTTTAGA AGGGCTTCGCACAAACCTAGCCTT
7078	Table 2	NA	494B11	-1	TCTGCTTGTCTCTCGTTTTGTT TATCTCCGCCGGCAGGGTCAG
7079	Table 1	NA	478E5	-1	GCTCTGAAACCCCTGGAACTCTTGAG CCTAAATGTATTTTAACATCTT
7080	Table 1	NA	478G6	-1	ATCTTGATGTGAAGCCCTTAAAAT AAACGTGAAGGTGCCAGCTTGCA
7081	Table 3A	NA	478H3	-1	ACCCAGCCTGATGTTCATCTTCTCC CCTCTTCATTTCTCTTGT
7082	Table 1	NA	478C7	-1	AGAAAAGACTAACACCAGAAATCATGC TGCAACACCAGAACATCCTTGG
7083	Table 1	NA	478G8	-1	TCACAAAATATGGCTCAAGGAGTATA AATCCCTCTCACGCACCCACAAA
7084	Table 1	NA	478H7	-1	ACTAACCAACCAATGAGAAATACTACT TACCTCCACCCATGCTGTGAACCC
7085	Table 3A	NA	479B4	-1	TGACCGCCTCAAAGACCAAAAGGACT CTACTCCATATTCTCTCACTGTC
7086	Table 1	NA	479D2	-1	GAATGACCACCTGACGCATTAGAGC TCACCTTCTGTTCTCAGCTGTT
7087	Table 1	NA	479G2	-1	TTGGTAGAAACCCACCCAAACCTAAAA TTCCCAAGCCTGACTGTCAGGCC
7088	Table 1	NA	479G3	-1	CATAAGTTGGTAGAAGAAATGGTGGT TTAAATCAGTAATATAGCTCCCC
7089	Table 1	NA	479G5	-1	TTCTCATCTCAATATCCCCAGAGCC CCAGTACCTCTAATACAAGACTT
7090	Table 1	NA	479G6	-1	CTATCAGGCCCTCAGATAGTCTTCT ATAAACCAATGATTCAAGTCAT
7091	Table 1	NA	479H4	-1	TACCCAAAGTCATTCCAGTAAGTCAT CTTTCTATTAGACTGGAAAGCTCC
7092	Table 1	NA	479H5	-1	GATGGTTCAGCAACTGAGGAGCTA GGGTGACGGGTCACAGAGCACAGA
7093	Table 1	NA	479H6	-1	AGAAAATTAGAAGATGACTACCATTG CTAAAGTCTATCCACATGCCAGCA
7094	Table 1	NA	479G12	-1	CCCCCTCGACCCCTCACACCTTTC CAGAGAGGCCCTAAAGATTCCCAT
7095	Table 1	NA	479H12	-1	TGTAAGGTTCTAAATTAGAGACC CTAGCCAGTCAGTGACAATATGCA
7096	Table 1	NA	482A5	-1	GAGTTGCTTATTCCAGTCTCTAAG ATATATCTCCCTTTAGTTGCTGAC
7097	Table 3A	NA	483G5	-1	TGGTGTAAATGAAACATGCCGTATTGCC TTATGGCCAGTTGAGTCCTTCC
7098	Table 1	NA	486C4	-1	AGGAAACCCAAAGAGTTAAACCAAG GCCACTATTTCATAGTCACACAA
7099	Table 1	NA	490F10	-1	GTGGTAATGAGAGCATTACAGACCA CCACACATGAGCTAAAATAATT
7100	Table 1	NA	493C2	-1	CCACCAAACCCACAGGCCGGACA AATGCAATACCATACAGAAACACAG
7101	Table 1	NA	58G4	-1	GGCCAAACCTTCTTACTCTGCCATT GTTCATGTCTTAATGAGCATGAA
7102	Table 3A	Hs.169370	DNA sequence from PAC 66H14 on chromosome 6q21-22. Contains FYN (P59-FYN, SYN, SLK) gene coding for two isoforms. Contains ESTs and STSs /cds=(12,1708)	-1	ATCAATCGGGCCTAATCCGAAGTCAGC AATCTTGCTATGAGTCCTTCCC

Table 8

7103	Table 1	NA		598H2	-1	TATTTTAAACAAAATCACACGGAAGG ATTCCCTCCGTCCCATGTGTTG
7104	Table 3A	NA	AA077131	1836605	7B08E10 Chromosome 7 Fetal Brain cDNA Library cDNA clone 7B08E10, mRNA sequence	-1 CAGATAGTGGTATTTGGGTGCTGGG CTTGCTGACCTGAGGAGGTGGCTG
7105	Table 3A	NA	AA501725	2236692	ng18e12.s1 NCI_CGAP_Lip2 cDNA clone IMAGE:929806 similar to contains Alu repetitive element; mRNA	-1 AACTCCATAGAGAAAGACTACGAATT TCGCTGGGAGGTAAAGGGAAAGC
7106	Table 3A	NA	AA501934	2236901	nh56a10.s1 NCI_CGAP_Pr8 cDNA clone IMAGE:956346, mRNA sequence	-1 GCATTTAGGAAAGACAGGTGAGTGTG CCACAACATACCTAACACATCAGCA
7107	Table 3A	NA	AA579400	2357584	nf33d05.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:915561 similar to contains Alu repetitive element;contains	-1 TTACTTGTCTCTCTCACCATCCTAA AACGTTGTTGCTGACATGAA
7108	Table 3A	NA	AF249845	8099620	isolate Siddi 10 hypervariable region I, mitochondrial sequence	-1 CCCCAGACGAAAATACCAAATGCATG GAGAGCTCCCGTAGTGGTTATA
7109	db mining	Hs.277051	AI630242	4681572	ad07c09.y1 cDNA /clone=ad07c09-(random)	-1 GCCTAAGTTCCAGAAGACTTTGACG ATGGAGAGCATGCAAAGCAGTAA
7110	db mining	Hs.277052	AI630342	4681672	ad08g11.y1 cDNA /clone=ad08g11-(random)	-1 TTTGCAGTTCAAGGATTGGTGGGAA ACGTTGTATGTGTTGGGTGGGG
7111	db mining	NA	AI732228	5053341	nf19e05.x5 NCI_CGAP_Pr1 cDNA clone IMAGE:914240 similar to contains Alu repetitive element, mRNA s	-1 AATAGATTCATTTCTTCCTCGAGT TAGTGGGTATTGGGACCTGAA
7112	Table 3A	NA	AW379049	6883708	RC3-HT0230-201199-013-c12 HT0230 cDNA, mRNA sequence	-1 CGACGGTGTCTGGAGTTCTGATGAG ACATGTAAGTAAGAGTTCTGTC
7113	Table 3A	Hs.232000	AW380881	6885540	UI-H-BI0-abh-h-06-0-Ul.s1 cDNA, 3' end /clone=IMAGE:2712035 /clone_end=3'	-1 ATATTCAAGCTGGCTGTGAAATTGG ATTTGAATTACCGGGATACATGCA
7114	Table 3A	Hs.325568	AW384988	6889647	602386081F1 cDNA, 5' end /clone=IMAGE:4514972 /clone_end=5'	-1 ACTGGTTTCATTCTAGTGTCCCCCA CCCGTCTAGTTCTATTTCTGT
7115	Table 3A	NA	AW836389	7930363	PM0-LT0030-101299-001-f08 LT0030 cDNA, mRNA sequence	-1 TTGGGAGTCACCAGGTTAAAGCAAAG CCTCAGTCACTGAAAGCAGAAACT
7116	Table 3A	NA	AW837717	7931691	CM2-HT0042-281299-062-e11 LT0042 cDNA, mRNA sequence	-1 TCTCTGTCTCAGAATTAGTGTATTG TTGGTGTCTAACCTGAAGTGGGA
7117	Table 3A	NA	AW837808	7931782	CM1-LT0042-100300-140-f05 LT0042 cDNA, mRNA sequence	-1 CATCTGCTCTGCTTCTCACACACTA GAAACACCACTGCCCATCCATG
7118	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence	-1 TCTGTGATTTATAACTGTTTTCAGGA AACGATCTTCCCACATGTGTTGA
7119	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	-1 TCATTCAGGCTTAATAAACACACTAA CCTCGCAGCACTGGAGCGTCTG
7120	Table 3A	NA	AW856490	7952183	PM4-CT0290-271099-001-c04 CT0290 cDNA, mRNA sequence	-1 AGCTTAGGATATCTTATTAGTGTTC GTTGGGCAAGAGGGCTAAAGGG
7121	Table 3A	NA	AW891344	8055549	PM2-NT0079-030500-001-a04 NT0079 cDNA, mRNA sequence	-1 TGGAACACACTGGCCCATTTATAG AGAAAAATAAAACATGATCCCCAT
7122	Table 3A	NA	BE061115	8405765	QV0-BT0401-011199-039-f09 BT0401 cDNA, mRNA sequence	-1 TTCCTTGATTTCACCAACCACACTAC GAAGGTGGCTTATGGTCTACAGCT
7123	Table 3A	NA	BE086076	8476469	PM2-BT0672-130400-006-h09 BT0672 cDNA, mRNA sequence	-1 TTCCACCACTTCAAGACTGGGGCA GGTAGAGAAAGACAAGCATAAGTACA
7124	Table 3A	NA	BE091932	8482384	IL2-BT0733-130400-068-C11 BT0733 cDNA, mRNA sequence	-1 TCTCTCTGCTTCCCACACCCCTCC CTTCTCTGCTTCCCACACCCCTCC
7125	Table 3A	Hs.173334	BE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922)	-1 CAGCACATCTCTGGTTTACAAGTTG GGTAATCATGAAAGCTGGAGATGC
7126	Table 3A	NA	BE163106	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence	-1 TATCTAAATTCTACCTTGTGATCCAA CTAGCTACCGTCTGGCACTGGCC
7127	Table 3A	Hs.301497	BE168334	8631159	arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544)	-1 TCCAATGCTCAAGTCACTCTGAGTCT TTGCTGGTGTCAACCTACAATGCC
7128	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453496 /clone_end=5'	-1 ACCTCACTATAGTAGCCATTAGGAA AGATGGGCCATACCAAATGGCT
7129	Table 3A	NA	BE177661	8656813	RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence	-1 AAGAACTATTCCCTTGAGAATTTCC TACTGGGAGTTACTGCTGTGATT
7130	Table 3A	NA	BE178880	8658032	PM1-HT0609-060300-001-g03 HT0609 cDNA, mRNA sequence	-1 TCTGTGTGAACATACATACAGGACTT TGATTCTACCTGTGCTGACCAT
7131	Table 3A	NA	BE247056	9098807	TCBAP1D6404 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA cDNA clone T mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	-1 GTGGAGCTGTGGCTTGTGATG CGGGCACTCTACACCTTCAGGTA
7132	Table 3A	Hs.11050	BE763412	10193336	mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	-1 TGTCACTGGCTCTCACTTGTGAA ATTGTTGCTTGGGAAAACACAG
7133	Table 3A	NA	BF330908	11301656	RC3-BT033-310800-115-f11 BT0333 cDNA, mRNA sequence	-1 GATGCAGTGGGTAGGGGTTGGGG TACAGACTGACTTGAGCTCGGAGTC
7134	Table 3A	NA	BF357523	11316597	CM2-HT0945-150900-379-g06 HT0945 cDNA, mRNA sequence	-1 TCAGGCACTCAAGTAAAGGCAAGACTT GAGTGTACATATAAGTCAGTTACA
7135	Table 3A	NA	BF364413	11326438	RC6-NN1068-070600-011-B01 NN1068 cDNA, mRNA sequence	-1 CCTGGGCTGAGTTGCTGCTCCTGA AGATTACAGTTGGTTAGAGAGA

Table 8

7136	Table 3A	NA	BF373638	11335663	MR0-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	-1	ACAGCAAACAAAGTGTCCAATCCTC TTAAACCCATTAAACCAAGAGTT
7137	Table 3A	NA	BF740663	12067339	QV1-HB0031-071200-562-h04 HB0031 cDNA, mRNA sequence	-1	AGTGCATTACACTGATGATAAACGA TAGTAGCTTCACAGGTTTGCTTCT
7138	Table 3A	NA	BF749089	12075765	MR2-BN0386-051000-014-b04 BN0386 cDNA, mRNA sequence	-1	AAGTGTGATTAGAAGCAGCTGGAAAGT ACGAGGAGGAGTGGAAAGTGTAGTCC
7139	Table 3A	NA	BF758460	12106380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	-1	CAGGAGTAAAACAGAGCTGGTGTGT GATACCTATGCTGGTGGAAAGCT
7140	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	-1	GGTGACTATCTTACCGGCTCCAGTA AACTCTGAAACATGTACCAAGCTAA
7141	Table 3A	NA	BF773393	12121293	CM2-IT0039-191200-638-h02 IT0039 cDNA, mRNA sequence	-1	GCTTGAAGATGTCTCAACAGAAAATC ACCGACATGAGGAAGCATCACGCT
7142	Table 3A	NA	BF805164	12134153	QV1-CI0173-061100-456-f03 CI0173 cDNA, mRNA sequence	-1	AGGAACATGGCTGCAGCATAATAAAAA GAATTGAATTCCATACTTTGTTAACCTG
7143	Table 3A	NA	BF818594	12156027	MR3-CI0184-201200-009-a04 CI0184 cDNA, mRNA sequence	-1	GGTGCTGCCATAGGTGCCAGTAAATG ACC GTTATGCGGAAATCAATTACA
7144	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08 HN0025 cDNA, mRNA sequence	-1	TGAAGTACTATAGGACTCAATGGGAC CAGTAGCAGCTCCAAGTGGATCAC
7145	Table 3A	NA	BF845167	12201450	RC5-HT1035-271200-012-F08 HT1035 cDNA, mRNA sequence	-1	ACACGGGACCTCCCTTGTATCTTCTG AGAATTAATAGAGATTTCATGCCA
7146	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119 cDNA, mRNA sequence	-1	CCAAAAGGAGAAAGATGACTAGGGT CACACTTGAGGATTGCCAGGGGG
7147	Table 3A	NA	BF875575	12265705	QV3-ET0100-111100-391-c02 ET0100 cDNA, mRNA sequence	-1	GCATCTCTTGAAGACGGGAACGT ACTTCAGGTTCTTCTGTGTTAGC
7148	Table 3A	NA	BF877979	12268109	MR0-ET0109-171100-001-b02 ET0109 cDNA, mRNA sequence	-1	GGCTCATTGGTTTAAAGTCTTCT ATGCCATCCCAGGGAGGAGGAT
7149	Table 3A	NA	BF897042	12288501	IL2-MT0179-271100-254-C11 MT0179 cDNA, mRNA sequence	-1	GACTGTGGACACCTCTACTGTGTC TCTTGCAGGCAAGCTACTGAC
7150	Table 3A	NA	BF898265	12289744	QV1-MT0229-281100-508-e11 MT0229 cDNA, mRNA sequence	-1	GCAGGGTGCGAGGCTCACAGCAGG TAGGAAAGTAACTAAGTGGAAAC
7151	Table 3A	NA	BF899464	12290923	IL5-MT0211-011200-317-f03 MT0211 cDNA, mRNA sequence	-1	CAGCTAAAGGCCGTAGGTCTATTGTGAC TGCCCTGGATGTGGATTACTCT
7152	Table 3A	NA	BF904425	12295884	CM1-MT0245-211200-662-d02 MT0245 cDNA, mRNA sequence	-1	CCAGAAATGCAGCCTACAGACCAAATA TCAATGGACTTGGTGTAGCCCTGC
7153	Table 3A	NA	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	-1	TTAAACACAGGCTGGAAAAGGAAG GAGAGGAGGGCATTTAGAGAAGA
7154	Table 3A	NA	BF926187	12323197	CM2-NT0193-301100-562-c07 NT0193 cDNA, mRNA sequence	-1	GTGGCTCGTAAATAGAACAGCAGT CACTGTGGAACCTACAAATGGCGA
7155	Table 3A	NA	BF928644	12326772	QV3-NT0216-061200-517-g03 NT0216 cDNA, mRNA sequence	-1	CACACCAAGCTGGCTGGGAGCAGA GGCTGCTGGTCTCATAGTAATCTAC
7156	Table 3A	NA	BG006820	12450386	RC4-GN0227-271100-011-d03 GN0227 cDNA, mRNA sequence	-1	TGGAGAAAATGAGAGACAGACAGTG AGTGAGAAAAGTCAGCGAAAAGGAAA
7157	Table 3A	NA	F11941	706260	HSC33F051 normalized infant brain cDNA cDNA clone c-33f05, mRNA sequence	-1	ACCTACTGTGAGATTATCCCCCTGT CTCCACACTGCCAGAAACTTACCA
7158	Table 3A	NA	U46388	1236904	HSU46388 Human pancreatic cancer cell line Patu 8988L cDNA clone xs425, mRNA sequence	-1	CCAAATGATACTAGGATTAAGCCCCA AAGCAAAGTCAGCACCACCATGG
7159	Table 3A	NA	U75805	1938265	HSU75805 Human cDNA clone f46, mRNA sequence	-1	TCCCAGAGCAACAACAAACACCCACTGA TAATGGACAACCAACACCCACTGA
7160	Table 3A	NA	W27656	1307658	36f10 Human retina cDNA randomly primed sublibrary cDNA, mRNA sequence	-1	CCACAGATGGCATGTAGTATTGAG ATTGAATCATCTGCTGTCCAGCC
7161	db mining	Hs.661	NM_004146	10764848	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18) (NDUFBT7), mRNA /cds=(22,435)	1	ACCTCATCCGGCTGCTCAAGTGAAG CGTGACGCTCCCAACTCTCTG
7162	db mining	Hs.943	NM_004221	4758811	natural killer cell transcript 4 (NK4), mRNA /cds=(59,763)	1	GACCTGGTGCTGTCGCCCTGGCATC TTAATAAAACCTGCTTAACTCTCC
7163	db mining	Hs.1063	NM_003093	4507126	small nuclear ribonucleoprotein polypeptide C (SNRPC), mRNA /cds=(15,494)	1	GCATAAGGAAGACTTGCTCCCTGTC CTATGAAAGAAATAGTTTGAG
7164	db mining	Hs.1321	NM_000505	9961354	coagulation factor XII (Hageman factor) (F12), mRNA /cds=(49,1896)	1	GGGACTCATTTCCCTCCCTGGTGA TTCCGCACTGAGAGACTGGCTGG
7165	db mining	Hs.288856	NM_003903	14110370	prefoldin 5 (PFDN5), mRNA /cds=(423,926)	1	AGACTGGATCGCACACCTTCAACA GATGTGTTCTGATTCCTGAAACCT
7166	db mining	Hs.1975	NM_030794	13540575	hypothetical protein FLJ21007 (FLJ21007), mRNA /cds=(257,2212)	1	AAGCAAATACCTTTACAAGTGAAG GAAGAATTTCTCTGCCGTCAA
7167	db mining	Hs.3804	NM_014045	13027587	DKFZP564C1940 protein (DKFZP564C1940), mRNA /cds=(565,1260)	1	GCACAAATGCTTCTATCCATAGCT ACGGCATTGCTCAGTAAGTGAAG
7168	db mining	Hs.3832	NM_032493	14210503	clathrin-associated protein AP47 (AP47), mRNA /cds=(76,1347)	1	TCCTGTAGAGGTTACAGCCTTTAT GCTGTTGAGCTCCAGGTACCAA
7169	db mining	Hs.4113	NM_006621	5729723	S-adenosylhomocysteine hydrolase-like 1 (AHCYL1), mRNA /cds=(47,1549)	1	GCCCACATTGGATTATAGTATAGCC TTCCCTCGACTCCCCACCAGACTTC
7170	db mining	Hs.83848	NM_000991	13904865	triosephosphate isomerase 1 (TPI1), mRNA /cds=(34,783)	1	AAGAGCTCTGAGCCCCCTGGCCCC AGAGCAATAAAGTCAGCTGGCTTC
7171	db mining	Hs.5076	AK025781	10438401	cDNA: FLJ22128 fis, clone HEP19543 /cds=UNKNOWN	1	GCTCAACATGGAAAGAAGGTACAGAA AGTGATGTGTTCAAAACATTAGCA

Table 8

7172	db mining	Hs.5298	NM_015999	7705760	CGI-45 protein (LOC51094), mRNA /cds=(182,1294)	1	TTATATACCTGGTCCCACATTCTTAG GCCCTGGATCTGCTTATAGAGCA
7173	db mining	Hs.5473	AW953785	8143468	602659796F1 cDNA, 5' end /clone=IMAGE:4802950 /clone_end=5'	1	GTTTACTCCGTCCTATCACTGGGTG GGCTGTGGGAAACCACTTATTGC
7174	db mining	Hs.5831	NM_003254	4507508	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1), mRNA /cds=(62,685)	1	GAACTGAAGCCTGCACAGTGTCCAC CCTGTTCCACTCCCATCTTC
7175	db mining	Hs.5890	BF698885	11984293	hypothetical protein FLJ23306 (FLJ23306), mRNA /cds=(562,930)	1	GAAGACCAAGAGAGACAACAGACGC AGCAACAGCCGAAGCACAGACAA
7176	db mining	Hs.6211	NM_015846	7710138	methyl-CpG binding domain protein 1 (MBD1), transcript variant 1, mRNA /cds=(139,1956)	1	AATTCAAGAAAATTGTTGGGAGGACAG CCCTTTTGTAACCTTGTGGGG
7177	db mining	Hs.6285	AL080220	5262711	mRNA; cDNA DKFZp586P0123 (from clone DKFZp586P0123); partial cds /cds=(0,1087)	1	TTTACCCAGCTCTGAAGGTATTGTT CTTGCCTGTGTTGAATAAAATCA
7178	db mining	Hs.6441	AL110197	58171115	mRNA; cDNA DKFZp586J021 (from clone DKFZp586J021) /cds=UNKNOWN	1	GTCTCTGATGCTTGTATCATTCTGA GCAATCGCTGGCTGGACAA
7179	db mining	Hs.6459	NM_024531	13375681	hypothetical protein FLJ11856 (FLJ11856), mRNA /cds=(239,1578)	1	GGTAAGCCCCCTGAGCCTGGGACCTA CATGTGGTTTGCCTAATAAAACATT
7180	db mining	Hs.6618	AL524742	12788235	AL524742 cDNA /clone=CS0DC008YI07-(5'-prime)	1	TCTGGCTCTGACCGGTTGATGCCCT GAGCGAATGAAATCATGAAATTGA
7181	db mining	Hs.6650	NM_007259	6005775	vacuolar protein sorting 45B (yeast homolog) (VPS45B), mRNA /cds=(33,1745)	1	TGCCCTACATAGCAATTCTGTGGC ACTGAGAAACCATGTATGACCACAA
7182	db mining	Hs.6763	NM_015310	7662395	KIAA0942 protein (KIAA0942), mRNA /cds=(52,1658)	1	GCAGTGTACTGTGCAATACCAAGG GCATAGCTCCCTGTAATTGGAA
7183	db mining	Hs.6780	NM_007284	6005845	protein tyrosine kinase 9-like (A6-related protein) (PTK9L), mRNA /cds=(104,1153)	1	CTGAGACTAGGGTCCCAGCACAGCC CAGAACCTTGGCCACAAGAAGTG
7184	db mining	Hs.6817	NM_025200	13376793	putative oncogene protein hlc14-06-p (HLC14-06-P), mRNA /cds=(51,635)	1	TCGCCTCCATGGTTTAAATGCAG TAAATAACATTCTGGATGAGACT
7185	db mining	Hs.7709	U79457	4205083	Homo sapiens, Similar to WW domain binding protein 1, clone MGC:15305 /clone=4309279, mRNA, complete cds /cds=(162,971)	1	GCTTTACCCCCCAGGACATACACAG GAGCCTTGTATCTCATTAAAGAGA
7186	db mining	Hs.7740	AF288741	14209837	oxysterol binding protein 2 (OSBP2), mRNA, complete cds /cds=(112,2748)	1	GGAATGTACCTCTCCCCAACACTGTT TTGTTAGCGAGCACCTTGTGACCA
7187	db mining	Hs.8108	NM_021080	10835268	disabled (Drosophila) homolog 1 (DAB1), mRNA /cds=(765,2426)	1	ACTCGCTCAGAAGAGGGAACTAACGC ATTTTGGCAACCAATGGCAGATA
7188	db mining	Hs.8109	NM_022743	12232400	hypothetical protein FLJ21080 (FLJ21080), mRNA /cds=(127,1236)	1	AGCTGTGTGAACTCTCTTATTGGAA ATTCTGTTCCGTGTTGTGAGGT
7189	db mining	Hs.8207	NM_020198	8910241	GK001 protein (GK001), mRNA /cds=(184,1635)	1	AGTCCCACATTTGGACCATGGCAG CTAAATTGTAACCTAACGATTCA
7190	db mining	Hs.226627	BC007375	13938462	leptin receptor short form (db) mRNA, complete cds /cds=(0,2690)	1	CTGCCCTCTCTGGACTTCGTGCCT TACTGAGTCTCTAACACTTTCT
7191	db mining	Hs.8768	NM_018243	8922711	hypothetical protein FLJ10849 (FLJ10849), mRNA /cds=(93,1382)	1	GGATAAACATTCTCATGAACCCACTG CCCCTCTGCATTTCCTCACTGGT
7192	db mining	Hs.8834	NM_006315	5454011	ring finger protein 3 (RNF3), mRNA /cds=(114,857)	1	CGCTTAAGAACATTGCCTCTGGGTGT CATGTGGACAGACTTCTGAATAG
7193	db mining	Hs.9683	NM_006260	5453979	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor (PRKRI), mRNA /cds=(690,2204)	1	GGGTTCAATCCCTCAGCTCAGGCG GACCATTAGATTTAAATTCCACCT
7194	db mining	Hs.9825	NM_016062	7706342	CGI-128 protein (LOC51647), mRNA /cds=(35,526)	1	GCTCCTGCCAGGGCTTACCGTTG TTCTTGAATCACTCACAAATGAGA
7195	db mining	Hs.10590	AL031685	9368423	DNA sequence from clone RP5-963K23 on chromosome 20q13.11-13.2 Contains a KRT18 (Keratin type I, Cytoskeletal 18 (Cytokeratin 18, CK18,CYK18)) pseudogene, the gene for a novel protein, the gene for spermatogenesis associated protein PD1 (KIAA0757) and the 3' end of the gene for KIAA0939 (novel Sodium/hydrogen exchanger family member). Contains ESTs, STSs, GSSs and four putative CpG islands /cds=(2,688)	1	AATCTGGCGAAACCTTCGTGAGGG ACTGATGTGAGTGTATGTCACCT
7196	db mining	Hs.11465	NM_004832	4758483	glutathione-S-transferase like; glutathione transferase omega (GSTLp28), mRNA /cds=(8,734)	1	GACTATGGGCTCTGAAGGGGCAGG AGTCAGCAATAAGCTATGTCGTAT
7197	db mining	Hs.11538	NM_005720	5031600	actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1B), mRNA /cds=(80,1198)	1	AGGGAGGGGACAGATGGGGAGCTTT TCTTACCTATTCAAGGAATACGTGC

Table 8

7198	db mining	Hs.12707	AK023168	10434970	cDNA FLJ13106 fis, clone NT2RP3002455, highly similar to mRNA for KIAA0678 protein /cds=UNKNOWN	1	ACCTTCTGAAAGCTCACAGTACACAT TAGTATGTATAACTGGCTTACCA
7199	db mining	Hs.12785	AL031685	9368423	DNA sequence from clone RP5-963K23 on chromosome 20q13.11-13.2 Contains a KRT18 (Keratin type I, Cytoskeletal 18 (Cytokeratin 18, CK18,CYK18)) pseudogene, a gene for a novel protein, the gene for spermatogenesis associated protein PD1 (KIAA0757) and the 3' end of the gene for KIAA0939 (novel Sodium/hydrogen exchanger family member). Contains ESTs, STSs, GSSs and four putative CpG Islands /cds=(0,1313)	1	TTTAAGGGAGTCAGGAATAGATGTAT GAACAGTCGTGTCACTGGATGCC
7200	db mining	Hs.13323	NM_022752	12232416	hypothetical protein FLJ22059 (FLJ22059), mRNA /cds=(783,1987)	1	CCACCTTCAACCTCTTAGCACTGGT GACCCAAAATGAAACCATCAAT
7201	db mining	Hs.13659	AL080209	5262698	Hypothetical protein DKFZp586F2423	1	AGACAGCAGTGTTAACATCTAAAT CGTGTGAGTCGTTATCTGCTCT
7202	db mining	Hs.14089	NM_013379	7019510	dipeptidyl peptidase 7 (DPP7), mRNA /cds=(0,1478)	1	ACCTCGACCTCAAGAGCCTCCACCC AGAAGATCCTGCTCCGTGGTTGAG
7203	db mining	Hs.16488	NM_004343	5921998	calreticulin (CALR), mRNA /cds=(68,1321)	1	GGGCAGTGGGCCCCAGATTGGCTCA CACTGAGAACTGAACTACAAC
7204	db mining	Hs.16580	NM_018303	8922829	hypothetical protein FLJ11028 (FLJ11028), mRNA /cds=(31,2355)	1	TGGCTTAAGTTCTAATTCAAGCG GTTTTGAAAAATTATGGCT
7205	db mining	Hs.109438	AB028950	5689390	clone 24775 mRNA sequence /cds=UNKNOWN	1	TGCAAGTTATAAGCCCCAACACAGGT CATGCTCAAATAAAATGATTCTA
7206	db mining	Hs.18586	NM_014826	7662135	KIAA0451 gene product (KIAA0451), mRNA /cds=(1482,2219)	1	CCAAACAATGATGTGGATTCTTTGC ACAGAAATTTAAGGTGGGATGG
7207	db mining	Hs.19575	NM_015941	7706261	CGL-11 protein (LOC51608), mRNA /cds=(233,1684)	1	ACAAAAGTCACCTGTTCTCTTTCA AACCAAAATTGGAGAAATTGTTG
7208	db mining	Hs.20529	AK025464	10437985	cDNA: FLJ21811 fis, clone HEP01037 /cds=UNKNOWN	1	GCTGGGACTCTAGCTCTGTGTTCA TAAAGACATTAAGAAGTGGATGGA
7209	db mining	Hs.20725	NM_020963	14211539	Mov10 (Moloney leukemia virus 10, mouse) homolog (MOV10), mRNA /cds=(70,3081)	1	GGAGAATGACACATCAAGCTGCTAAC AATTGGGGAGGGGAAGGAAGAA
7210	db mining	Hs.343590	AB011104	3043587	601471579F1 cDNA, 5' end /clone=IMAGE:3874747 /clone_end=5'	1	ACCTGGTTAACACAGCTCACATCA CTGAATGTACACATGAGTTAAA
7211	db mining	Hs.23449	NM_018842	10047119	insulin receptor tyrosine kinase substrate (LOC55971), mRNA /cds=(333,1553)	1	CTTAAGGACGCCCTTGCCTGGCCCT TTATTACAGCCAACACGGTAGGC
7212	db mining	Hs.23990	NM_017838	8923443	nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs) (NOLA2), mRNA /cds=(86,547)	1	TCCATCAGTGCCTTCCATGTAGAAC TAAAGGCTGTTCCAAGAATGTGGG
7213	db mining	Hs.24024	NM_015376	7662333	KIAA0846 protein (KIAA0846), mRNA /cds=(272,2341)	1	ATCTGAAAGCACTCAGAAGGCAGCC ATCCCAGATGTTGGTTCATGTA
7214	db mining	Hs.334842	BC008330	14249901	tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA /cds=(67,1422)	1	TGGTTAGATTGTTTCACTTGGTAT CATGTCCTTCCATGTGACCTGT
7215	db mining	Hs.24641	AK022982	10434687	cDNA FLJ12920 fis, clone NT2RP2004594 /cds=(96,2144)	1	CATGTCCTTGGAAACATGATAAGTTAC ATACACAGTTCTCCACACAT
7216	db mining	Hs.321105	NM_015462	7661683	cDNA: FLJ21737 fis, clone COLF3396 /cds=UNKNOWN	1	AGGTTTACATGAAACCTGTTCTAGGC TGTTGGACATTGGTGTGGAGAGTT
7217	db mining	Hs.26802	NM_021158	11056039	protein kinase domains containing protein similar to phosphoprotein C8FW (LOC57761), mRNA /cds=(294,1370)	1	GACACTTGGGTCCACAATCCAGG TCCATACTCTAGGTTGGATACCA
7218	db mining	Hs.26892	NM_018456	8922098	uncharacterized bone marrow protein BM040 (BM040), mRNA /cds=(357,749)	1	AGAAATGATTTGCAGCTGAGTGAATC AGGAAGTGACAGTGTGACTGAAG
7219	db mining	Hs.27076	NM_003729	4506588	RNA 3'-terminal phosphate cyclase (RPC), mRNA /cds=(170,1270)	1	TCTGAGAGATGGACAATGAAATATC AGTTGGTGGATATGTGTGATAGCT
7220	db mining	Hs.27445	NM_016209	7706428	unknown (LOC51693), mRNA /cds=(58,480)	1	CTTCAGGGCAGGCAGCTGTGCTG TTCTCTCAACTAAAGGTCTTGAG
7221	db mining	Hs.27633	NM_015456	7661663	DKFZP586B0519 protein (DKFZP586B0519), mRNA /cds=(75,1199)	1	GCTGGACACACGGTGAAGATTTCTCG TATGTAATAAAAGGCAATTGGT
7222	db mining	Hs.28310	BG260891	12770707	602372491F1 cDNA, 5' end /clone=IMAGE:4480510 /clone_end=5'	1	CTCAACGAAAGGCTCACACTAACAGG GGAGGATTACAGCACCACAATACT
7223	db mining	Hs.28914	NM_000485	4502170	adenine phosphoribosyltransferase (APRT), mRNA /cds=(71,813)	1	CCACACTGAACCCAATTACACACAGC GGGAGAACCGCAGTAAACAGCTTC
7224	db mining	Hs.29893	AL133426	6562628	mRNA full length insert cDNA clone EUROIMAGE 146397 /cds=UNKNOWN	1	AGGCCCTGGAAAATTGTGCTTCCA ACGTGGCCTTCAATTCTTGCTTT
7225	db mining	Hs.30120	BF970066	12337281	602272333F1 cDNA, 5' end /clone=IMAGE:4360233 /clone_end=5'	1	TATTAAGCTTGGCCAGGCTCTGTTC ATGAAGGTTCCCCCAGCGGTGGCC

Table 8

7226	db mining	Hs.30250	AF055376	3335147	short form transcription factor C-MAF (c-maf) mRNA, complete cds /cds=(807,1928)	1	GCTATACCACTGACTGTATTGAAAAC CAAAGTATTAAGAGGGAAACGCC
7227	db mining	Hs.30443	AL136599	13276698	mRNA; cDNA DKFZp564G1816 (from clone DKFZp564G1816); complete cds /cds=(137,3091)	1	TGGGGTCAGTTAACGCCTCAGTATTCTTAGCTTTGTTGATTTGGCACT
7228	db mining	Hs.31137	NM_006504	5729992	protein tyrosine phosphatase, receptor type, E (PTPRE), mRNA /cds=(51,2153)	1	ATGGTGCAAACCCCTGGAACAGTATGA ATTCTGCTACAAAGTGGTACAAGA
7229	db mining	Hs.34114	NM_000702	4502270	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 (+) polypeptide (ATP1A2), mRNA /cds=(104,3166)	1	AGAACGAGCGAGTCATGGCTAAT TATCATCAATCTTATGTATTGTT
7230	db mining	Hs.35254	NM_020119	9910221	hypothetical protein FLB6421 (FLB6421), mRNA /cds=(310,792)	1	GGAATGTTGCTGTGGGGATTCTATT GTAACCTCTCTGTGAACGTCTCA
7231	db mining	Hs.38735	BG149337	12661367	nad26g06.x1 cDNA, 3' end /clone=IMAGE:3366730 /clone_end=3'	1	ATGCCAAATCCCTGACACGTGGCCTT TGAAAATACCATGGAACGTTCCA
7232	db mining	Hs.41322	AI655467	4739446	tt13b01.x1 cDNA, 3' end /clone=IMAGE:2240617 /clone_end=3'	1	ACATTCTGACTCCATCTGCGGCCCTCA TTAAGGTATAGAAAACATACTAGG
7233	db mining	Hs.42346	AY013295	11693027	calcineurin-binding protein calsarcin-1 mRNA, complete cds /cds=(131,925)	1	ATGATAATGTTGGCATCTGTGATAAAA CTATCAATGAGGCCTCCATCATGC
7234	db mining	Hs.42699	AW956580	8146278	EST368665 cDNA	1	AGACTCACATGTAGAAAAGCCTCCAG TATTAAGCTCTGAATTCTTCTCT
7235	db mining	Hs.44131	AB023191	45B9591	mRNA for KIAA0974 protein, partial cds /cds=(0,1697)	1	ATGGCAACAATGCTGACAGCAAGCA GTAGATCCTCTGATTCCAATTACCA
7236	db mining	Hs.44441	BE295812	9179366	601176827F1 cDNA, 5' end /clone=IMAGE:3532039 /clone_end=5'	1	GGAAACCTCATTAATTAGACAAAGAA CACCAAGGCTATGACCACAGCAGC
7237	db mining	Hs.46919	AY007155	9956067	clone CDABP0095 mRNA sequence /cds=UNKNOWN	1	GGCTCACCAGAGTACCCAGAAAT CAGTATGGAATTAGAGGACAGTGGC
7238	db mining	Hs.56009	NM_006187	5453823	2'-5'-oligoadenylate synthetase 3 (100 kD) (OAS3), mRNA /cds=(34,3297)	1	ATCCCAGGCCCTCAGTCTTGGCAAT GGCCACCCCTGGTGTGGCATATTG
7239	db mining	Hs.57843	W63785	1371386	zd30g09.s1 cDNA, 3' end /clone=IMAGE:342208 /clone_end=3'	1	GCATACATAAGGCAAAGAATGACAA AAGGCTTAATCCACCTAGAAGACA
7240	db mining	Hs.58373	BF339748	11286202	602034942F1 cDNA, 5' end /clone=IMAGE:4182851 /clone_end=5'	1	ATATAGTGGAGACAAAACACAGGAG GCGGGGGATATCATGTAGCAGAGC
7241	db mining	Hs.59236	NM_032139	14149802	hypothetical protein DKFZp434L0718 (DKFZP434L0718), mRNA /cds=(133,3285)	1	TCTATGTGCCTGGATATGTCCAA ATGATGGAAAAGAAACAGTAAACT
7242	db mining	Hs.62406	NM_024660	13375912	hypothetical protein FLJ22573 (FLJ22573), mRNA /cds=(99,1166)	1	GCTTGGCTCATCTGGGTTTGCCTGG GCTAACACCCAATAAGAACTTGT
7243	db mining	Hs.63042	NM_018457	8922156	DKFZp564J157 protein (DKFZP564J157), mRNA /cds=(77,523)	1	CTGCGGTTTGGAACCTTACCTCTCC TCCTTAGCCAAATATGCTGTCTTG
7244	db mining	Hs.65648	NM_005105	4826971	RNA binding motif protein 8A (RBM8A), mRNA /cds=(12,536)	1	TCCAGGCCATTTCAGGGACTCTGA AGTACCTTGTAGTAGTAAATGCT
7245	db mining	Hs.339868	NM_003974	4503358	oh47h10.s1 cDNA, 3' end /clone=IMAGE:1469827 /clone_end=3'	1	TGGCAGCCAGGAACCTGAGTATGACA ATGTTGACTAAAGAAGGCCAA
7246	db mining	Hs.75056	NM_003938	4501976	adaptor-related protein complex 3, delta 1 subunit (AP3D1), mRNA /cds=(203,3547)	1	AGAGAGAGACATATCACGCTGCTGTC ATGATTTGTGTCAGATGATCCA
7247	db mining	Hs.75082	NM_001665	4502218	ras homolog gene family, member G (rho G) (ARHG), mRNA /cds=(129,704)	1	CTTCTGGGACCTTCCTACCCCCAT CAGCATCAATAAAACCTCTGTCT
7248	db mining	Hs.75309	NM_001961	4503482	eukaryotic translation elongation factor 2 (EEF2), mRNA /cds=(0,2576)	1	TAGATGATTCTAGCAGGCAGGAAGT CCTGTGGGTGTCACCATGAGCAC
7249	db mining	Hs.75725	NM_003564	4507356	transgelin 2 (TAGLN2), mRNA /cds=(73,672)	1	CCATGGCTCTGGGCTTGAGGAAGAT GAGTTGTTGATTAAATAAGAAT
7250	db mining	Hs.75770	NM_000321	4506434	retinoblastoma 1 (including osteosarcoma) (RB1), mRNA /cds=(138,2924)	1	AGGTCAAAGGCCTACTATTCCTGGGT CTTTGCTACTAAGTCACATTAG
7251	db mining	Hs.75780	NM_002642	4505794	phosphatidylinositol glycan, class C (PIGC), mRNA /cds=(293,1186)	1	TTTCTGGGACCTCTTGATTACATG CTGTAACATATGAAGTGATGTGGT
7252	db mining	Hs.76057	NM_000403	9945333	galactose-4-epimerase, UDP- (GALE), mRNA /cds=(76,1122)	1	TGGCACAAAACCTCTCCCTCCAGGC ACTCATTTATATTGCTCTGAAAGA
7253	db mining	Hs.76662	NM_032327	14150105	hypothetical protein MGC2993 (MGC2993), mRNA /cds=(158,1048)	1	TGAGGTCACTGCCACTTCTCACATGC TGCTTAAGGGAGCACAAATAAAGG
7254	db mining	Hs.77268	NM_002826	13325074	quiescin Q6 (QSCN6), mRNA /cds=(75,2318)	1	CACGCTACCCCCCTGCCTTGGAGGT GTGTGGAATAATTATTTTGTAA
7255	db mining	Hs.77290	NM_008755	5803186	transaldolase 1 (TALDO1), mRNA /cds=(50,1063)	1	AATGCAGAGAATGAAAGTAGCGCAT CCCTGAGGCTGACTCCAGATCTG
7256	db mining	Hs.77805	NM_001696	4502316	ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 31kD (ATP6E), mRNA /cds=(75,755)	1	GTGGCACACCACTCCTTCCAGCAGTA GTCGCTTACTGTTACCTGTTAG
7257	db mining	Hs.78592	NM_001414	4503502	eukaryotic translation initiation factor 2B, subunit 1 (alpha, 26kD) (EIF2B1), mRNA /cds=(10,927)	1	AGCAACAGTATTCTGCATGGTTCACT GCTTAAGAAAATGCCTCTGGAAAT

Table 8

7258	db mining	Hs.78605	BC006159	13544048	Homo sapiens, clone IMAGE:3635549, mRNA, partial cds /cds=(0,891)	1	AAACATGTCCCTGGAGAGTAGCCTGC TCCCACACTGTCACTGGATGTCAT
7259	db mining	Hs.78890	AF171938	5852969	NUMB isoform 1 (NUMB) mRNA, complete cds /cds=(270,2225)	1	CAGTTGCAGCCTCTTGACCTCGGATA ACAATAAGAGAGCTCATCTCATTT
7260	db mining	Hs.79150	NM_006430	5453604	chaperon containing TCP1, subunit 4 (delta) (CCT4), mRNA /cds=(0,1619)	1	TGGGCTTGGTCTCCAGTTGGCATTT GCTGAAGTTGATTGAAACAAATT
7261	db mining	Hs.79259	NM_016404	7705476	hypothetical protein (HSPC152), mRNA /cds=(35,412)	1	TTCTGCCGTGTGATCCCCAACCTT GACCCAAATGACACCAAACACAGTG
7262	db mining	Hs.79356	NM_006762	5803055	Lysosomal-associated multispanning membrane protein-5 (LAPTM5), mRNA /cds=(75,863)	1	TGTGTCGACAGGGAGGAAGTTCA ATAAGCAACACAAGCTTCAAGGA
7263	db mining	Hs.79572	NM_001909	4503142	cathepsin D (lysosomal aspartyl protease) (CTSD), mRNA /cds=(2,1240)	1	CTCCCCTTGGCGGCTGAGAGCCCC AGCTGACATGAAATACAGTTGTG
7264	db mining	Hs.81337	NM_009587	6806889	lectin, galactoside-binding, soluble, 9 (galectin 9) (LGALS9), transcript variant long, mRNA /cds=(56,1123)	1	CTCCACCACCTGACCAGAGTGTTC TTCAGAGGACTGGCTCCCTTCCA
7265	db mining	Hs.82030	NM_004184	7710155	tryptophanyl-tRNA synthetase (WARS), mRNA /cds=(187,1602)	1	CTCTGCCCTCTGTCAACCACTAGAG TAAATAAACTCTTGGCTCTAA
7266	db mining	Hs.82396	NM_016816	8051620	2',5'-oligoadenylate synthetase 1 (40-46 kD) (OAS1), transcript variant E18, mRNA /cds=(33,1235)	1	AAATTCCAGCCTGACTTCTCTGT GCACCTGATGGGAGGGTAATGTC
7267	db mining	Hs.82933	BC008739	14250568	Homo sapiens, protein x 013, clone MGC:3073 IMAGE:3346340, mRNA, complete cds /cds=(101,325)	1	CTGTAGGCCAGGGTGGAAATGAAGTC AGCTCCTTTATAGTTGAAATACA
7268	db mining	Hs.83753	NM_003091	4507124	small nuclear ribonucleoprotein polypeptides B and B1 (SNRBP), mRNA /cds=(0,695)	1	TTGGCGGGCCATCCAACAGGTGAT GACCCCCACAAGGAAGAGGTACTGTT
7269	db mining	Hs.85838	NM_004207	4759111	solute carrier family 16 (monocarboxylic acid transporters), member 3 (SLC16A3), mRNA /cds=(62,1459)	1	GGAAGATGAAATAACCTGCGTGTG GGTGGAGTGTCTCGTGCCGAATT
7270	db mining	Hs.306565	NM_013341	9558756	clone HQ0688 /cds=UNKNOWN	1	AGTGAGGACAATGTGGCTTGCCTT TTGAATCTACAGATAATGCGATGT
7271	db mining	Hs.89497	NM_005573	5031876	lamin B1 (LMNB1), mRNA	1	GAGGGTGGGGAGGGAGGTGGAGG GAGGGAAAGGTTCTCTATTTAAATG
7272	db mining	Hs.89525	NM_004494	4758515	hepatoma-derived growth factor (high-mobility group protein 1-like) (HDGF), mRNA /cds=(315,1037)	1	TGCTGACTGTAGCTTGGAAAGTTAG CTCTGAGAACCGTAGATGATTTCA
7273	db mining	Hs.92208	NM_003815	11497001	a disintegrin and metalloproteinase domain 15 (metargidin) (ADAM15), mRNA /cds=(7,2451)	1	GATTGAGGAAGGTCCGACAGCTG TCTCTGCTCAGTTGCAATAACCGTG
7274	db mining	Hs.103527	NM_003975	4503632	SH2 domain protein 2A (SH2D2A), mRNA /cds=(86,1255)	1	GATTCTGTCTGGCTAATAATCATCA CCAACTGCCTTCTCCTACAGGGA
7275	db mining	Hs.104679	BF347362	11294957	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds /cds=(2206,2373)	1	AGATTCTTAGGGCACGTTGTTCCCC TTGGAGGTTTCCACACCGAGTC
7276	db mining	Hs.105749	AB011125	3043629	mRNA for KIAA0553 protein, partial cds /cds=(0,3289)	1	GCCATACTCTGGCTGCCTTTGCCT TCCTAGGGGCATTCTTAACTT
7277	db mining	Hs.105751	AL138761	8573811	DNA sequence from clone RP11-16H23 on chromosome 10. Contains the gene KIAA0204 (HSLK) for a protein kinase, the COL17A1 gene for collagen type XVII alpha 1 (BP180), ESTs and GSs /cds=(0,3557)	1	TGCTCTTATCTACTTGAGAGCAAC TGCTTTCAATCATGGATTGAC
7278	db mining	Hs.324406	AK026741	10439662	ribosomal protein L41 (RPL41), mRNA /cds=(83,160)	1	TGGACCTGTGACATTCTGGACTATTT CTGTGTTTATTTGTGGCCGAGGT
7279	db mining	Hs.108371	NM_001950	12669914	E2F transcription factor 4, p107/p130-binding (E2F4), mRNA /cds=(62,1303)	1	TGAAGGTGTCTGTGACCTCTTGATG TGCGCTTCTCAACCTCTGACTGA
7280	db mining	Hs.109760	NM_002491	4505360	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12) (NDUFB3), mRNA /cds=(252,548)	1	CCTGGAGTCCCTGAATAAGATAAGA AGCATCACTGAAGATAATAACCTGG
7281	db mining	Hs.109857	AF151783	14248494	MEG3 (MEG3) mRNA, complete cds /cds=(52,2253)	1	TTGTCGGAGATTTGCGCCTTAGT GCTTTTGAGGGGTTCCCATCATC
7282	db mining	Hs.306417	NM_014714	7662193	cDNA FLJ10935 fis, clone OVARC1000661 /cds=(250,936)	1	CTGCTAGGCTCTGCCACCGGCCAC CAACACTCCTGTAACTTCAATAAAG
7283	db mining	Hs.114199	BG621594	13672965	602617003F1 cDNA, 5' end /clone=IMAGE:4730856 /clone_end=5'	1	TTAAAATACTGTCAATTGGTGGGAGG GGATTGCAATTGATTAGTCCA
7284	db mining	Hs.118788	BF131637	10970677	601820457F1 cDNA, 5' end /clone=IMAGE:4052246 /clone_end=5'	1	CTCACACACGCAGCGACAGTCAGA ACAAAACAGGAACAAAGCTACAACAC
7285	db mining	Hs.122559	NM_024872	13376307	hypothetical protein FLJ22570 (FLJ22570), mRNA /cds=(0,1490)	1	TGAATAGTGTGCAAGACTCACAGATAA TAAGCTCAGAGCACTCCCGCA
7286	db mining	Hs.123373	AW883279	8153115	602853825F1 cDNA, 5' end /clone=IMAGE:4994982 /clone_end=5'	1	CCCACTGCTCACGAAGTTAAAGGA AGATCTGCTGGTAGTGTAGTCT

Table 8

7287	db mining	Hs.125078	AF090094	4063629	clone IMAGE 172979 /cds=UNKNOWN	1	CGAGCCGACCATGTCTTCATTGCTT
7288	db mining	Hs.130740	AK000315	7020316	cDNA FLJ20308 fis, clone HEP07264 /cds=(90,1226)	1	CCACAAGAACCGCGAGGACAGAGC
7289	db mining	Hs.132955	AL132665	6137021	mRNA; cDNA DKFZp566E034 (from clone DKFZp566E034); complete cds /cds=UNKNOWN	1	TTTCCCCCTTAAAGTCTCCCTGGCTTT
7290	db mining	Hs.133230	BC000085	12652672	Homo sapiens, ribosomal protein S15, clone MGC:2295 (IMAGE:3507983, mRNA, complete cds /cds=(14,451)	1	TCCCTTCCCTCCCTCTCCACT
						1	AACCCGTTGTGAAATTATGGATT
						1	AACTGAGCAAAGTGATTATGCAT
7291	db mining	Hs.142677	AK024108	10436406	cDNA FLJ14046 fis, clone HEMBA1005461 /cds=UNKNOWN	1	GCCCCCGATCTACACCC TGAGCCT
7292	db mining	Hs.146170	NM_022842	12383093	hypothetical protein FLJ22969 (FLJ22969), mRNA /cds=(274,2223)	1	CAGAGCACTGCTACTTTTAAATA
7293	db mining	Hs.146550	Z82215	3135984	DNA sequence from clone RP1-68O2 on chromosome 22 Contains the 5' end of the APOL2 gene for apolipoprotein L 2, the APOL gene for apolipoprotein L, the MYH9 gene for nonmuscle type myosin heavy chain 9. ESTs, STSs and GSSs /cds=(0,5882)	1	AAGCGTCTCATGGAGTTGGACTGGT
7294	db mining	Hs.149846	NM_002213	4504772	integrin, beta 5 (ITGB5), mRNA /cds=(29,2419)	1	TGGGGTGATAAATTTGTTCTTT
7295	db mining	Hs.151738	NM_004994	4826836	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) (MMP9), mRNA /cds=(19,2142)	1	AAGCCAGGCTTGGGATACAAGTTCT
7296	db mining	Hs.336451	NM_024519	13375657	Nucleoside diphosphate kinase type 6 (inhibitor of p53-induced apoptosis-alpha)	1	TTCTCTCCAGCCATCCCTT
7297	db mining	Hs.154276	NM_001186	4502352	BTB and CNC homology 1, basic leucine zipper transcription factor 1 (BACH1), mRNA /cds=(118,2328)	1	GGATACAAACTGGTATTCTGTTCTGG
7298	db mining	Hs.155975	NM_005608	5032004	protein tyrosine phosphatase, receptor type, C-associated protein (PTPRCAP), mRNA /cds=(63,683)	1	AGGAAAGGGAGGAGTGGAGGTGG
7299	db mining	Hs.159410	NM_014484	7657338	mtolybdopterin synthase sulfurylase (MOCS3), mRNA /cds=(2,1384)	1	TGAAGGTACATCGTTGCAAATGTGA
7300	db mining	Hs.160999	AV648418	9869432	AV648418 cDNA, 3' end /clone=GLCBJC04 /clone_end=3'	1	GTTTCTCTGTTATTTTATTTACAGAGTT
7301	db mining	Hs.164036	NM_002076	4504060	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease III D) (GNS), mRNA /cds=(87,1745)	1	GGACACTCAGTCACATTAACAACT
7302	db mining	Hs.164478	NM_022461	11968002	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2 (FLJ21939), mRNA /cds=(379,1557)	1	CTGCCCCTGCCCAGCCACATCCCTT
7303	db mining	Hs.169615	NM_023080	12751496	hypothetical protein FLJ20989 (FLJ20989), mRNA /cds=(52,741)	1	GGATAACAAACTGGTATAGTCTGA
7304	db mining	Hs.171811	AK023758	10435787	cDNA FLJ13696 fis, clone PLACE2000140 /cds=UNKNOWN	1	TGCACTGAGCTTCTGAGCTTCTG
7305	db mining	Hs.171992	NM_002843	4506314	protein tyrosine phosphatase, receptor type, J (PTPRJ), mRNA /cds=(349,4362)	1	TCATCACAGTGTGGTAAGGTTGCAAA
7306	db mining	Hs.173373	AB023148	4589505	mRNA for KIAA0931 protein, partial cds /cds=(0,2204)	1	TTCAAAACATGTACCCCTTAAGTCCT
7307	db mining	Hs.173638	NM_030756	13540470	transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA /cds=(307,2097)	1	ACACTGATTAGGCTCCGGTTTCCCTT
7308	db mining	Hs.177534	NM_007207	13518225	dual specificity phosphatase 10 (DUSP10), mRNA /cds=(142,1590)	1	GGCTTCTGCTTTCACTGTAATGGC
7309	db mining	Hs.177592	NM_001003	4506668	602761378F1 cDNA, 5' end /clone=IMAGE:4896908 /clone_end=5'	1	CTAGGAGTTTCATTATGCTTCCTGT
7310	db mining	Hs.179661	BC008791	14250651	Homo sapiens, tubulin, beta 5, clone MGC:4029 IMAGE:3617988, mRNA, complete cds /cds=(1705,3039)	1	ACAGTAGCTTACAGAGCTTCTG
7311	db mining	Hs.179986	NM_005803	6552331	flotillin 1 (FLOT1), mRNA /cds=(184,1447)	1	TCAGTGTGGCTTCTGCTACATTAGT
7312	db mining	Hs.180859	NM_016139	7705850	16.7kD protein (LOC51142), mRNA /cds=(81,536)	1	GGCTTCTTAAACTAGCTGTTATGT
7313	db mining	Hs.181301	AK024855	10437263	cDNA: FLJ21202 fis, clone COL00293 /cds=UNKNOWN	1	AACCTAAACGTATTTCACTAACTCTG
7314	db mining	Hs.181311	NM_004539	7262387	asparaginyl-tRNA synthetase (NARS), mRNA /cds=(73,1719)	1	GCTCCTTCTCCATAAAAGCACATT
7315	db mining	Hs.181391	AL390158	9368848	mRNA; cDNA DKFZp761G2113 (from clone DKFZp761G2113) /cds=(0,564)	1	CCACCAAATGCATGTATGTATTCTC
7316	db mining	Hs.182281	NM_016407	7705482	hypothetical protein (HSPC164), mRNA /cds=(70,990)	1	AATAGGCTGTATCCAGCAGTC

Table 8

7317	db mining	Hs.183180	NM_016476	13324711	anaphase promoting complex subunit 11 (yeast APC11 homolog) (ANAPC11), mRNA /cds=(0,398)	1	CAACAAGGTGAAACAAGGGCTGGA GCTCGTGTGTTGCCATCACTAT
7318	db mining	Hs.183593	NM_006965	5902161	zinc finger protein 24 (KOX 17) (ZNF24), mRNA /cds=(164,1270)	1	GAGCATTCCAGGGGAGGTACCT GTGAGGTTCCAGAACACTGTAGTTT
7319	db mining	Hs.184029	AL137509	6808164	Homo sapiens, clone MGC:2764 IMAGE:2958229, mRNA, complete cds /cds=(70,1785)	1	TGCAGGTGTTGACAAGATCCGCCATC TGTAATGTCCGGCACAATAAAA
7320	db mining	Hs.187652	AA833892	2907491	od84g04.s1 cDNA /clone=IMAGE:1372758	1	AAGAGTCTGACTTCTCACTAGGAGCA TGTCTGTTGACTTACTTCAAACA
7321	db mining	Hs.188751	BG111638	12605142	602282682F1 cDNA, 5' end /clone=IMAGE:4369892 /clone_end=5'	1	CAAACACCAACCAAGATAACACCGG AACGATAAACAGCAGAACAGAGA
7322	db mining	Hs.193392	U46120	1184779	expressed unknown mRNA /cds=UNKNOWN	1	TGGGTTGTCAGTTCAAGGCTAGATG TGCATCATGGCAGGAAGAAAGAAG
7323	db mining	Hs.195453	NM_001030	4506710	ribosomal protein S27 (metallopanstimulin 1) (RPS27), mRNA /cds=(35,289)	1	AAGGATGTTCTTCAGGAGGAAGCA GCACTAAAAGCACTTGAGTCAGAAG
7324	db mining	Hs.196914	D86976	1504025	mRNA for KIAA0223 gene, partial cds /cds=(0,3498)	1	CGGAAGCCACCGTGTGGTTCTTCAC AGGACAGTTATTGGCTGAAATA
7325	db mining	Hs.198281	NM_002654	4505838	pyruvate kinase, muscle (PKM2), mRNA /cds=(109,1704)	1	CCTCCACTCAGCTGTCCCTGCAGCAA CACTCCACCCCTCACCTCCATT
7326	db mining	Hs.200317	AB037825	7243188	mRNA for KIAA1404 protein, partial cds /cds=(64,5841)	1	TCCCTCTCCAGTGTCTCTAGAAC AGACATTTAGGTATCTCAGGTCT
7327	db mining	Hs.202613	BG284262	13035032	602407238F1 cDNA, 5' end /clone=IMAGE:4519449 /clone_end=5'	1	CAGCCGCAGCATAAACGAACAACA GAGGAGAACGACGAGGACAGAGTT
7328	db mining	Hs.210778	AL136679	12052881	mRNA; cDNA DKFZp564C1278 (from clone DKFZp564C1278); complete cds /cds=(104,1690)	1	TCACTGGATTTCTGTCCTCACTAG AACACCATTGTCTCATCTCATATTGA
7329	db mining	Hs.2111594	NM_006503	5729990	proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4), mRNA /cds=(12,1268)	1	GCTCTCTCGCACCCCCCAGCACCTCT GTCCCCAAACCTCATCCCTTTT
7330	db mining	Hs.226307	NM_004900	4758159	phorbol (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA /cds=(79,651)	1	AGCTGCTCACAGACACCAGCAAAGC AATGTGCTCTGATCAAGTAGATT
7331	db mining	Hs.326048	NM_006319	5453905	cDNA FLJ14186 fis, clone NT2RP200526 /cds=UNKNOWN	1	ATGCTCATGTTGTCCCCACCGCC CACTTGTGATGTCACTGACTGTC
7332	db mining	Hs.227835	NM_014972	14149658	KIAA1049 protein (KIAA1049), mRNA /cds=(96,2126)	1	GCTGAGTGTGTCGCTCCCTGGTCCA CTGTTCTCCTATAATGTAATGTTGG
7333	db mining	Hs.231867	NM_014423	7656878	ALL1 fused gene from 5q31 (AF5Q31), mRNA /cds=(337,3828)	1	TGAGCACATTGATAAGATGGTTCC GTGAGCTATGATAAGATTGAAATT
7334	db mining	Hs.232400	NM_031243	14043071	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(169,1230)	1	ATAAATATGCAGTGATATGGCAGAG ACACCAAGAGCAGATGCAGAGAGCC
7335	db mining	Hs.236131	NM_022740	13430859	homeodomain-interacting protein kinase 2 (HIPK2), mRNA /cds=(108,3704)	1	TTGAACCGGGAAAGTGGGAGGACGTA GAGCAGAGAAGAGAACATTTTAA
7336	db mining	Hs.343556	AF090896	6690168	clone HO0131 PRO0131 mRNA, partial cds /cds=(0,233)	1	TTTGCTCATTCTAAACTCAAGCTTTA AGCCTCACAGAAATTACAGGGGT
7337	db mining	Hs.238936	BG538032	13530264	602563534F1 cDNA, 5' end /clone=IMAGE:4688193 /clone_end=5'	1	GCCATAGGCTTACATGGGGCATACTC GTTACACAGTCAGAATGTTGAAA
7338	db mining	Hs.241412	NM_030882	13562089	apolipoprotein L_2 (APOL2), mRNA /cds=(477,1490)	1	GGTCTCTGCTCTGTCTTCCAGCAT CCACTCTCCCTGTCTCTGGGG
7339	db mining	Hs.241471	AL133642	6599293	mRNA; cDNA DKFZp586G1721 (from clone DKFZp586G1721); partial cds /cds=(0,659)	1	TCAGCACCAAGTCATGTTAAAGAC CAGAGAGACAAGCATTTGCCAAG
7340	db mining	Hs.245188	NM_000362	9257248	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA /cds=(1183,1818)	1	CGAACCTGTCTAGAAGGAATGTATT TTGCTAAATTCTGAGCTACTGT
7341	db mining	Hs.249170	NM_012476	7110734	ventral anterior homeobox 2 (VAX2), mRNA /cds=(32,904)	1	CAAATGGCTTGGTCCCAGCTTGT GTGCGTGAGTGCAGTGTGAGTGT
7342	db mining	Hs.258551	NM_012100	6912247	aspartyl aminopeptidase (DNPEP), mRNA /cds=(151,1578)	1	CTCTGGAAAGACTTCTGCCCCATCC CTGGCACCTGAGAGGGGAAGTC
7343	db mining	Hs.259412	BG772376	14083029	602722490F1 cDNA, 5' end /clone=IMAGE:4839143 /clone_end=5'	1	GGCGCGGTGACCCACTTATGGGACT TGGCCTTCTTGTGTTGTTAA
7344	db mining	Hs.259577	AW665292	7457838	hj02c11.x1 cDNA, 3' end /clone=IMAGE:2980828 /clone_end=3'	1	ACCCAGTTCATGATTACTCTACTCTT AACACTCAATCCCCCTAATTAAACC
7345	db mining	Hs.259679	AW956608	8146291	EST368878 cDNA	1	TTCGATAAACAGCGTTGACTTGCTTG TACCACTTAAGAGTTGTGAGTGCT
7346	db mining	Hs.265827	NM_022873	13259549	interferon, alpha-inducible protein (clone IFI-6-16) (G1P3), transcript variant 3, mRNA /cds=(107,523)	1	TCCAGAACCTTGTCTATCACTCTCC CAACAAACCTAGATGTGAAACAGA
7347	db mining	Hs.265891	AK001503	7022798	cDNA FLJ10641 fis, clone NT2RP2005748 /cds=UNKNOWN	1	GGGATCTTCAAATGGATGTGAGTT GCCTTTCTATAGGTGACAATCA

Table 8

7348	db mining	Hs.266456	AW768693	7700715	hk65e11x1 cDNA, 3' end /clone=IMAGE:3001580 /clone_end=3'	1	AGAGCAAGCATTACAGAAAATAGGTC TGAAGACAGGAAAGACAAAGA
7349	db mining	Hs.267368	NM_017842	8923451	hypothetical protein FLJ20489 (FLJ20489), mRNA /cds=(482,1201)	1	ATGTGTCCTGCCCTCAGCTTTGC CTTATCTGTCACTGTCATTTA
7350	db mining	Hs.267812	NM_003794	4507144	sorting nexin 4 (SNX4), mRNA /cds=(0,1352)	1	TCTGTGAATTGAAATTCTCTCAATC AAAGTCCCCAACAGAACACA
7351	db mining	Hs.272027	NM_012177	6912365	F-box only protein 5 (FBXO5), mRNA /cds=(61,1404)	1	AGGTCCCCCTGCTGGTACAAAGAAAA GCAAAAAGAATTACGAAGATTGT
7352	db mining	Hs.272534	AL080068	5262475	mRNA; cDNA DKFZp564J062 (from clone DKFZp564J062) /cds=UNKNOWN	1	GCCAGAACATAATTACAGAGACG AGAACAGGGTGTGGGAGAGAGGAA
7353	db mining	Hs.273415	NM_000034	4557304	aldolase A, fructose-bisphosphate (ALDOA), mRNA /cds=(167,1281)	1	TCTTCTTCCTCGTGACAGTGGTGT GTGGTGTGTCGTGAATGCTAAG
7354	db mining	Hs.273830	AK022804	10434416	cDNA FLJ12742 fis, clone NT2RP2000644 /cds=UNKNOWN	1	CAGTCAAACATTACCTTGTGCCTT GGCTCACTCTGTGCCTTTCTCCA
7355	db mining	Hs.274287	AK001508	7022805	cDNA FLJ10646 fis, clone NT2RP2005773, highly similar to pyrroline 5-carboxylate reductase isoform mRNA /cds=UNKNOWN	1	ACAGGAAACGGGCTTCTCTGAATTG GTAATGGAAAAGAAGTGAGCAC
7356	db mining	Hs.275163	NM_002512	4505408	non-metastatic cells 2, protein (NM23B) expressed in (NME2), nuclear gene encoding mitochondrial protein, mRNA /cds=(72,530)	1	GTCCTGGACACAGCTCTTCATTCCA TTGACTTAGAGGCAACAGGATTGA
7357	db mining	Hs.276818	AI435118	4300940	th95e09,x1 cDNA, 3' end /clone=IMAGE:2126440 /clone_end=3'	1	ACCTCGCCACAAGATTCTGCAATCT CCTAAAGTACAGATGAGAAAGGAA
7358	db mining	Hs.278582	AF135794	4574743	AKT3 protein kinase mRNA, complete cds /cds=(0,1439)	1	TGCCAAGGGTTAATGAAACAAATAG CTGTTGACGTTGCTCATTTAAGA
7359	db mining	Hs.279535	AK027035	10440049	cDNA: FLJ23382 fis, clone HEP16349 /cds=UNKNOWN	1	CAGTGGCACACCTAACCGACTA ATTTCACTGTTGTAAAGTGAATT
7360	db mining	Hs.283007	NM_008227	5453913	phospholipid transfer protein (PLTP), mRNA /cds=(87,1588)	1	CCCAGTGCACAGAGAACGGGAT TTGAAGCTGTACCCAATTAAATTCC
7361	db mining	Hs.283565	NM_005438	4885242	FOS-like antigen-1 (FOSL1), mRNA /cds=(34,849)	1	TGAGCCCTACTCCCTGCAGATGCCAC CCTAGCCAATGTCCTCCCTCC
7362	db mining	Hs.284296	AK026646	10439543	cDNA: FLJ22993 fis, clone KAT11914 /cds=UNKNOWN	1	GCAGGGAGGGAGGATAAGTGGAT CTACCAATTGATTCTGGAAACAAACAA
7363	db mining	Hs.284892	AF246229	10419514	AF246229 cDNA /clone=RB82	1	GGCAACTACCTTGTGGAAACAAAG CATAGGGAGTGAAGTGTCTAAA
7364	db mining	Hs.284893	AF246230	10419515	AF246230 cDNA /clone=RB16	1	GCTGGCCGATCTCCCCACAGTT GCAAGAACGATTTCAAAGAAATAGT
7365	db mining	Hs.285280	AK024885	10437298	cDNA: FLJ21232 fis, clone COL00752 /cds=UNKNOWN	1	ATTGGGATGAAACTACTTTAGCAAAG TCACAGATCAGAACACAGACCGT
7366	db mining	Hs.288038	NM_006625	12056474	TLS-associated serine-arginine protein 1 (TASR1), mRNA /cds=(72,623)	1	AGGAGACTGGGTGCTATAATTAGATT ATTTTAGGGCAGACAGAGAGCTGT
7367	db mining	Hs.288283	AK026008	10438707	cDNA: FLJ22355 fis, clone HRC06344 /cds=UNKNOWN	1	AGCCTGCAAGGTTAGGACTTGAAGA GGGAAGGTATTTAAACTGGCGA
7368	db mining	Hs.289043	AL136719	12052956	mRNA; cDNA DKFZp566G0346 (from clone DKFZp566G0346); complete cds /cds=(278,790)	1	TTAGTGAGTTGGAATGAATGTTGAT AGGTCAGAGGTTCTCGTGTTCACA
7369	db mining	Hs.289087	AK024468	10440449	mRNA for FLJ00061 protein, partial cds /cds=(0,522)	1	TCACCTCTCAGTTGAAAGATTCTCT TTGAAAGGTCAAGACCGTGACT
7370	db mining	Hs.290494	BF475245	11544422	EST 003 cDNA, 5' end /clone_end=5'	1	AGTCTGGATGTAAGGCCCTGCCTCAA GAGACACTATGGGAGGGAAACAA
7371	db mining	Hs.290874	BE730505	10144599	60156267F1 cDNA, 5' end /clone=IMAGE:3832302 /clone_end=5'	1	AAAGGAAGAAGCACGATGCAAACAG AAACAAGACGAGACAGAGTGAGCGA
7372	db mining	Hs.332403	NM_024113	13129129	hypothetical protein MGC4707 (MGC4707), mRNA /cds=(72,1067)	1	ACTGCTTCAAGTCTGACCCCTTGT GCTTAATAGCTAACAAACATGTG
7373	db mining	Hs.292998	AW972292	8162138	EST384381 cDNA	1	AACAAATAGGAATAAGGTTACTTCAGC CTTAAGGGCTTATCATACTGCTG
7374	db mining	Hs.293984	NM_032323	14150097	hypothetical protein MGC13102 (MGC13102), mRNA /cds=(161,1345)	1	GACAGGGAAATCTGCCAACAGAG GGGTGTGTCTTGTGCCACA
7375	db mining	Hs.295362	AK027365	14041993	cDNA FLJ14459 fis, clone HEMBP002409 /cds=UNKNOWN	1	AACAAGTCCATGACTCCCAAGGGTT AAGGACCAATGGTTCACTGAGACA
7376	db mining	Hs.297964	BF838049	12187621	RC1-HT0975-161100-011-g07 cDNA	1	ACACTCATCATATGACTGCTC AGTCGAACGGACTGCAGTCGTT
7377	db mining	Hs.299329	AK000770	7021066	cDNA FLJ20763 fis, clone COL09911 /cds=UNKNOWN	1	TACTGCTATGGAATGAGACCAACT TCTCCTGTGTCTCCCTCAGCTTC
7378	db mining	Hs.300631	AK022958	10434851	cDNA FLJ12896 fis, clone NT2RP2004194, weakly similar to Rattus norvegicus Golgi SNARE GS15 mRNA /cds=UNKNOWN	1	TGCCAAGTGAAGACAAACTGCTAGG CTGTATCCATAATTCAGGTAG
7379	db mining	Hs.301417	M80899	178282	novel protein AHNAK mRNA; partial sequence /cds=(0,3835)	1	AAACCGACCGCCTGTAGGCTCTGG AACTATACAGATAAGGTAAGAGTC
7380	db mining	Hs.301612	NM_005253	4885244	FOS-like antigen 2 (FOSL2), mRNA /cds=(3,983)	1	GACCAATCATCAGACTCCTTGAAC CCCCACTCTGCTGGCTCTGTAACC
7381	db mining	Hs.301636	NM_000287	4505728	peroxisomal biogenesis factor 6 (PEX6), mRNA /cds=(70,3012)	1	AGAGATCCAGGTGCAAGTGATTGA GACAGCAGCAACAGCTCAAGAGATA

Table 8

7382	db mining	Hs.337774	NM_004723	4758671	rho/rac guanine nucleotide exchange factor (GEF) 2 (ARHGEF2), mRNA /cds=(112,2988)	1	ATGCCCCTTCTCCTCTCCCTCTTC CTCTTACTGCTGTTCTCCCTTCT
7383	db mining	Hs.318568	BF475243	11544420	EST 001 cDNA, 5' end /clone_end=5'	1	ACATCCATAGAACATAACATCAAAGT TGTGAAGTGTGCAAGGGGAGGGC
7384	db mining	Hs.318569	BF475244	11544421	EST 002 cDNA, 5' end /clone_end=5'	1	AGCACTTACTGTCAGGCATTCAAGAT GTGAGCAATGACAATAATTACCT
7385	db mining	Hs.321709	NM_002560	4505548	purinergic receptor P2X, ligand-gated ion channel, 4 (P2RX4), mRNA /cds=(27,1193)	1	AATCTGATTGAGTCTCCACTCCACAA GCACTCAGGGTCCCCAGCACCTC
7386	db mining	Hs.322478	D38491	559327	mRNA for KIAA0117 gene, partial cds /cds=(0,683)	1	AACCCAAGAAAAGAGTTGCTCTTACT ATCTACTGCTGACTCTTGAACCTT
7387	db mining	Hs.323114	AK023846	10435906	cDNA FLJ13784 fis, clone PLACE4000593 /cds=UNKNOWN	1	TTCTGAGGTGGCTTTTCCATACAGA GCTGGCTCATACACCAATAAAAGT
7388	db mining	Hs.323949	NM_002231	13259537	kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody Ia4)) (KAI1), mRNA /cds=(181,984)	1	AGGGGGCTGGACTTCTACCTGCC TCAAGGGTGTATATTGTATAGGG
7389	db mining	Hs.324507	NM_024524	13375687	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(182,2056)	1	TGTGTCAGAATGGCACTAGTTCAGTT TATGTCCTTCTGATATAGTAGCT
7390	db mining	Hs.326447	BC004857	13436058	Homo sapiens, clone IMAGE:3690478, mRNA, partial cds /cds=(0,71)	1	CTATCAGCCCCAAGTGGAGCAGAAC AGAGGGATTGGGAGGAATGTCCTC
7391	db mining	Hs.333558	BG577468	13592532	gu.seq cDNA	1	TGCTAAGGAGAGGGGCCATGAAGAG TTTGTGAGAACATCGTGTCTGAG
7392	db mining	Hs.334303	BG642392	13777102	gu.seq395250 cDNA	1	AGTCAGAACCTCAAGTCCCCATTAAA GGGGCTGAAAATACAAGTACAGT
7393	db mining	Hs.334804	NM_000558	6715603	hemoglobin, alpha 1 (HBA1), mRNA /cds=(37,465)	1	CTCCCTTCTGCACCCGTACCCCC GTGGTCTTGAATAAAAGTCTGAGTG
7394	db mining	Hs.334853	NM_032241	14149953	hypothetical protein FLJ23544 (FLJ23544), mRNA /cds=(125,517)	1	CAGATGGTGTGGGTCAAGTACATC CCCAGTCGTGGCCCTTGGACAG
7395	db mining	HS.250655	NM_032695	14249283	Prothymosin, alpha (gene sequence 28)	1	TTTGGCTGTGTTGATGTATGTGTA AACATGTTGTCACAAATAAACAA
7396	db mining	Hs.336689	AA493477	2223318	ESTs	1	AGCTTAGGTGACAGAGCAAGACTCC ATTTCAAAACAAAAACAAAAACAAA
7397	db mining	Hs.180450	BF791433	12096487	ribosomal protein S24 (RPS24), transcript variant 1, mRNA /cds=(37,429)	1	ACACTGAGAATACACGACATACACGC ACCGACAAAGACAAACACAGACAGC
7398	Table 3A	NA	AA077131	1836605	7B08E10 Chromosome 7 Fetal Brain cDNA Library cDNA clone 7B08E10, mRNA sequence	1	CAGCCACCTCTCAGGTCAAGACAAG CCCAGCACCCAAATACCAACTATCTG
7399	Table 3A	NA	AA501725	2236692	ng18e12.s1 NCI_CGAP_Lip2 cDNA clone IMAGE:929806 similar to contains Alu repetitive element; mRNA	1	GGCTTCCCTATTACCTCCAGCGAA TTCGTAGTCTTCTATGGAGTT
7400	Table 3A	NA	AA501934	2236901	nh56a10.s1 NCI_CGAP_Pr8 cDNA clone IMAGE:956346, mRNA sequence	1	TGCTGATGTGTTAGGTAGTTGTGGCA CACTCACCTGTCCTTCTAAATGC
7401	Table 3A	NA	AA579400	2357584	nf33d05.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:915581 similar to contains Alu repetitive element;contains	1	TTCATGCTCAGCAAAACACGTTTA GGATGGTAGAGAGAACAAAGTAA
7402	Table 3A	NA	AF249845	8099620	isolate Siddi 10 hypervariable region I, mitochondrial sequence	1	TATTAACCACTCACGGAGCTCTCCA TGCATTGGTATTTCTGCTCTGGGG
7403	db mining	Hs.277051	AI630242	4681572	ad07c09.y1 cDNA /clone=ad07c09-(random)	1	TTACCTGCTTGCATGCTCTCCATCG TCAAAAGTCTCTGGAAACTTAGGC
7404	db mining	Hs.277052	AI630342	4681672	ad08g11.y1 cDNA /clone=ad08g11-(random)	1	CCCCACCCAAACACATACAAACGTTT CCCAACATCTGAACTGCAAAA
7405	db mining	NA	AI732228	5053341	nf19e05.x5 NCI_CGAP_Pr1 cDNA clone IMAGE:914240 similar to contains Alu repetitive element; mRNA s	1	TTCAAGGTCCCAATACCCAACAACT CGAAGGAAGAAATGGAAATCTATT
7406	Table 3A	Hs.197803	AW379049	6883708	mRNA for KIAA0160 gene, partial cds /cds=(0,2413)	1	TGCACAGAACTCTTACTTACATGTCT CATCGAAACTCCAGAACACCCTCG
7407	Table 3A	Hs.232000	AW380881	6885540	UI-H-B10-p-abh-h-06-0-UI.s1 cDNA, 3' end /clone_end=IMAGE:2712035	1	TGCATGTATCCCGGTAACTCAATCC AATTTCACAGCCACTGCTGAATAT
7408	Table 3A	Hs.325568	AW384988	6889647	602388081F1 cDNA, 5' end /clone_end=IMAGE:4514972 /clone_end=5'	1	TACAGGAAAATGAAACTAGACGGGTG GGGGGACACTAGAAATGAAAACCAAGT
7409	Table 3A	NA	AW836389	7930363	PM0-LT0030-101299-001-f08 LT0030 cDNA, mRNA sequence	1	AGTTTCTGCTTCAGTGAATGAGGCT TTGCTTAACTCTGGTGAATCCCAA
7410	Table 3A	NA	AW837717	7931691	CM2-LT0042-281299-062-e11 LT0042 cDNA, mRNA sequence	1	TCCCACTTCAAGTTAACGCACCAAAAGC AATCACTAATTCTGGACACAGGA
7411	Table 3A	NA	AW837808	7931782	CM1-LT0042-100300-140-f05 LT0042 cDNA, mRNA sequence	1	CATGGATGGGGCAGTGGTGTCT AGTGTGTGAGGAAGCAGAGCAGATG
7412	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence	1	TCACCCACAGATGGGAAGATCGTTCC TGAAACAGTCTATAATCACAGA
7413	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	1	CAGACGCTCCAGTGTGCCAGGTT AGTGTGTTATTAGACCTGAAATGA

Table 8

7414	Table 3A	NA	AW856490	7952183	PM4-CT0290-271099-001-c04 CT0290 cDNA, mRNA sequence	1	CCCTTTAGGCCCTCTGCCCCAACAGT GAACACTAAATAGATATCTTAAGCT
7415	Table 3A	NA	AW891344	8055549	PM2-NT0079-030500-001-a04 NT0079 cDNA, mRNA sequence	1	ATGGGGATCATGTTTATTTCTCTA TATAATGGGCCAGTGTGTTCCCA
7416	Table 3A	NA	BE061115	8405765	QV0-BT0041-011199-039-f09 BT0041 cDNA, mRNA sequence	1	AGCTGTAGACCATAAGGCCACCTCAG GTAGTGGTTGGGAATCAACCAA
7417	Table 3A	NA	BE086076	8476469	PM2-BT0672-130400-006-h09 BT0672 cDNA, mRNA sequence	1	TGTACTTATGCTGTCTCTACCTG CCCCCAGTCCTGAAGTGGTGAA
7418	Table 3A	NA	BE091932	8482384	IL2-BT0733-130400-068-C11 BT0733 cDNA, mRNA sequence	1	GGAGGGTGTGGGAAGCAAGAGAAGA ACATTCTGTAGGGCAGAGAAAGAA
7419	Table 3A	Hs.173334	BE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922)	1	GCATCTCCAGCTTCATAGTTACCCA ACTTGTAAACCGAAGATGTGCTG
7420	Table 3A	NA	BE163106	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence	1	GGCCAGTGCCAGACGGTAGCTAGTT GGATGCTAAAGGAGAATTAGATA
7421	Table 3A	Hs.301497	BE168334	8631159	arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544)	1	GGCATTGTAGGTTGACACCCAGCAAAG ACTCAGAGTACTTGAGCATTGGA
7422	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453466 /clone_end=5'	1	AGCCCATTGGATATGGCCCATCTTT ACCTAATGGCTACTATAGTGAGGT
7423	Table 3A	NA	BE177661	8656813	RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence	1	AATCACAGCAGTAACCTCCAGTAGGA AAGATTCTCAAAGGAATAGTTCTT
7424	Table 3A	NA	BE178880	8658032	PM1-HT0609-060300-001-g03 HT0609 cDNA, mRNA sequence	1	AATGGTCAGGCACAGGTAGAACAA GTCCTGTATGTATGTTCACACAGA
7425	Table 3A	NA	BE247056	9098807	TCBAP1D6404 Pediatric pre-B cell acute lymphoblastic leukemia Baylor- HGSC project=TCBA cDNA clone T mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	1	TACCTGAAGGTAGAGAGTGCCCG CATCCAGCAAGGCCAACAGCTTCCAC
7426	Table 3A	Hs.11050	BE763412	10193336	RC3-BT0333-310800-115-f11 BT0333 cDNA, mRNA sequence	1	CTGTGTTTCCCAAAGCAACAATTTC AAACAAAGTGAGAGCCACTGACA
7427	Table 3A	NA	BF330908	11301656	RC3-BT0333-310800-115-f11 BT0333 cDNA, mRNA sequence	1	GACTCCGAGCTCAAGTCAGTGTAC CCCCAACCCCTAACCCACTGCATC
7428	Table 3A	NA	BF357523	11316597	CM2-HT0945-150900-379-g08 HT0945 cDNA, mRNA sequence	1	TGTAACGTACTTTATGTATCACTCAAG TCTTCGCTTACTGTAGTGCTG
7429	Table 3A	NA	BF364413	11326438	RC6-NN1068-070600-111-B01 NN1068 cDNA, mRNA sequence	1	TCTCTTAACCAAAACTGTAATCTCA GGACCAAGCAAACACTAGGCCAAGG
7430	Table 3A	NA	BF373638	11335663	MR0-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	1	AACTCTTGGTTAAATGGGTTAATAGA GGATTTGAAACACTTGTGCTGT
7431	Table 3A	NA	BF740663	12067339	QV1-HB0031-071200-562-h04 HB0031 cDNA, mRNA sequence	1	AGAACGAAACCTGTGAAGCTACTATC GTTTATCATCAGTGTGAATGCACT
7432	Table 3A	NA	BF749089	12075765	MR2-BN0388-051000-014-b04 BN0386 cDNA, mRNA sequence	1	GGACTAACCTCACCTCTGCTAC TTCCAGCTGCTCTTAATCACACTT
7433	Table 3A	NA	BF758480	12106380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	1	AGTCTTCCACCCAGCATAGGTATCAC ACAACCCAGCTGTCTTACTCTG
7434	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	1	TTAGCTGGTACATTGTTAGAGTTA CTGGGAGCCGGTAAGATAGTCACC
7435	Table 3A	NA	BF773393	12121283	CM2-IT0039-191200-638-h02 IT0039 cDNA, mRNA sequence	1	AGCGTGTAGCTCTCATGTCGGTGA TTTCTGTGAGACATCTTCAAGC
7436	Table 3A	NA	BF805164	12134153	QV1-CI0173-051100-456-f03 CI0173 cDNA, mRNA sequence	1	ACAAAAGTATGGAATTCAATTCTTTT ATATGCTGCAGCCATGTTCTGCCCT AGA
7437	Table 3A	NA	BF818594	12156027	MR3-CI0184-201200-009-a04 CI0184 cDNA, mRNA sequence	1	TGTAATTGATTTCCGCATAAACGGTC ATTACTGGCACCTATGGCAGCAC
7438	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08 HN0025 cDNA, mRNA sequence	1	GTGATCCACTTGGAGCTGCTACTGGT CCCATTGAGTCTTATAGTACTTC
7439	Table 3A	NA	BF845167	12201450	RC5-HT1035-271200-012-F08 HT1035 cDNA, mRNA sequence	1	TGCCATGAAATCTTATTAATTCTCAG AAAGATCAAAGGAGGTCCCGTGT
7440	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119 cDNA, mRNA sequence	1	CCACCTGGCAAATCCTCAAGTGTGA CCCTAGTCATCTTCTCTCTT
7441	Table 3A	NA	BF875575	12265705	QV3-ET0100-111100-391-c02 ET0100 cDNA, mRNA sequence	1	GCTAAACAGAAAAGAACCTGTAGTAC AGTTCCCGTCTCAAAGAAGATGC
7442	Table 3A	NA	BF877979	12268109	MR0-ET0109-171100-001-b02 ET0109 cDNA, mRNA sequence	1	ATCCTCCTCCCCCTGGGATGGCATAGA AGAGACTTAAACCAAATGAG
7443	Table 3A	NA	BF897042	12288501	IL2-MT0179-271100-254-C11 MT0179 cDNA, mRNA sequence	1	GTCAGTAAGCTGCCTGCCAACAG ACACAGTGGAGGTGTCCACAGTC
7444	Table 3A	NA	BF898285	12289744	QV1-MT0229-281100-508-e11 MT0229 cDNA, mRNA sequence	1	GTTCGCACTTGTAGTTACTCTCTTAC TGCTGTAGCTCTGCACCCCTGC
7445	Table 3A	NA	BF899464	12290923	IL5-MT0211-011200-317-f03 MT0211 cDNA, mRNA sequence	1	AGAGTAATCCACATCCCAGGGACAGT CACAATGACCTACGGCTTAGCTG
7446	Table 3A	Hs.324473	BF804425	12295884	40 kDa protein kinase related to rat ERK2 /cds=(134,1180)	1	GCAGGGCTACACCAAGTCCATTGATA TTTGTCTGTAGGTCTGCATTCTGG
7447	Table 3A	NA	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	1	TCTTCTCTAAATGCCCTCCTCTCT CCTTTTCCAGACCTGGTTAAA
7448	Table 3A	Hs.104679	BF926187	12323197	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds /cds=(2206,2373)	1	TCGCCATTGGTAGTTCCACAGTGC TGCTCTTCTATTTACGAAGGCCAC
7449	Table 3A	Hs.75703	BF928644	12326772	small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386)	1	GTAGATTACTATGAGACCCAGCAGCT CTGCTCCAGCCAGCTGTGGTGTG

Table 8

7450	Table 3A	NA	BG006820	12450386	RC4-GN0227-271100-011-d03 GN0227 cDNA, mRNA sequence	1	TTCCCTTTCGCTGACTTCTCACTCA CTGTCTGTCCTCATTTCTCCA
7451	Table 3A	NA	F11941	706260	HSC33F051 normalized infant brain cDNA cDNA clone c-33f05, mRNA sequence	1	TGGTAAGTTCTGGCAGTGTTGGAGAC AGGGAAATAATCACAACAGTAGGT
7452	Table 3A	NA	U46388	1235904	HSU46388 Human pancreatic cancer cell line Pato 8986t cDNA clone xs425, mRNA sequence	1	CCATGGTGGTCTTGACTTGCCTTG GGCCTTAATCTAGTATCATTTGG
7453	Table 3A	NA	U75805	1938265	HSU75805 Human cDNA clone f46, mRNA sequence	1	TCAGTGGGTGTTGGTTGCCATTAGT TGAGACTTAGTTGTTGCTCTGGGA
7454	Table 3A	NA	W27656	1307658	36110 Human retina cDNA randomly primed sublibrary cDNA, mRNA sequence	1	GGCTGGACAGCAGATGATTCAAATCT CAATACTACATGCCCATCTGTGG
7455	literature	NA	X17403	59591	Human cytomegalovirus strain AD169 complete genome	1	AATAATAGATTAGCAGAAGGAAATAAT CCGTGCGACCGAGCTTGTGCTTCT
7456	literature	NA	X17404	59591	Human cytomegalovirus strain AD169 complete genome	1	TTTTGCGAACCTTTAGGAACCAAGCAA GTCAACAAAAGACTAACAAAGAAA
7457	literature	Hs.2799	X17405	59591	Cartilage linking protein 1	1	GAGATCGACATCGTCATCGACCGAC CTCCGCAACCCCTACCCAAATCC
7458	literature	Hs.2159	X17406	59591	mRNA for cartilage specific proteoglycan	1	ACATTCAAAGTTGAGCGTCTTCAT GTACGCCGTTCGGCCTCACAGAG
7459	literature	NA	X17407	59591	Human cytomegalovirus strain AD169 complete genome	1	CCAACGACACATCCACAAAATCCC CATCGACTCTCACAAATCGCATCAT
7460	literature	NA	X17408	59591	Human cytomegalovirus strain AD169 complete genome	1	CTTGAGCAGGTCTCAAGGCTGTAA CTAACGTGCTGTGCCCCGTCTTC
7461	literature	NA	X17409	59591	Human cytomegalovirus strain AD169 complete genome	1	GATGTCGGTCTACGGCGCTATCGGCC ATCATCGGATCTATCTGCTCTACC
7462	literature	NA	X17410	59591	Human cytomegalovirus strain AD169 complete genome	1	TCTTCTGGGACGCCAACGACATCTAC CGCATCTCGCCGAATTGGAAGGC
7463	literature	NA	X17411	59591	Human cytomegalovirus strain AD169 complete genome	1	ACGAACAGAAAATCTCAAAGACGCTG ACCCGATAAGTACCGTCACGGAGA
7464	literature	NA	X17412	59591	Human cytomegalovirus strain AD169 complete genome	1	AGAGAACAAACAAACCACCAACGACGA TGAACACAAACGCTCAACCAAACA
7465	literature	NA	X17413	59591	Human cytomegalovirus strain AD169 complete genome	1	CTGCATCGTCGTCCTCCTCCCTCT CGGAGATCCGACGGAGAACAAAC
7466	literature	NA	X17414	59591	Human cytomegalovirus strain AD169 complete genome	1	CTGAGCCTGGCCATCGAGGCAGCCA TCAGGACCTGAGGAACAAAGTCTCA
7467	literature	NA	X17415	59591	Human cytomegalovirus strain AD169 complete genome	1	CCTCTGGAGGCAAGAGCACCCACCC TATGGTACTAGAACGAAGGCTGAC
7468	literature	NA	X17416	59591	Human cytomegalovirus strain AD169 complete genome	1	TTCGTGGGACCCAAGTTGCGAAGAA CTACACTGTCCTGGCGAGTT
7469	literature	NA	J01917	209811	Adenovirus type 2, complete genome	1	CTGTGGAAATGTATCGAGGACTTGCTT AACGAGTCGGCAACCTTGGAC
7470	literature	NA	J01918	209811	Adenovirus type 2, complete genome	1	GCTGGCCTGCACCCGCGCTGAGTT GGCTCTACGGATGAAGATAACAGATT
7471	literature	NA	J01919	209811	Adenovirus type 2, complete genome	1	GGGGCGGTTAGGCTGTCTCCCTTCT CGACTGACTCCATGATCTTTCTG
7472	literature	NA	J01920	209811	Adenovirus type 2, complete genome	1	TGTTTGCTTATTATTATGTGGCTTAT TTGTTGCTAAACGCGCAGACCGG
7473	literature	Hs.250596	J01921	209811	xy45f10.x1 cDNA, 3' end /clone=IMAGE:2856139 /clone_end=3'	1	ACGGTGTAACTATAAGCTATGTGGT GGTGGGGCTATACTACTGAATGAA
7474	literature	NA	J01922	209811	Adenovirus type 2, complete genome	1	TTTCTGCCCTGAAGGGCTTCCCTCCCT CCCAATGGGGTTAAACATAAAT
7475	literature	NA	J01923	209811	Adenovirus type 2, complete genome	1	GGCTTATGCCCATGATCTGAACATC CAGAGTCACCTTACCACTGCTCTG
7476	literature	NA	J01924	209811	Adenovirus type 2, complete genome	1	CTACTGCCGTACAGCGAAAGCCGCC CCAACCCGCGAAACGAGGAGATG
7477	Table 3A	NA	AA077131	1836605	7B08E10 Chromosome 7 Fetal Brain cDNA Library cDNA clone 7B08E10, mRNA sequence	-1	CAGATAGTGTATTGGGTGCTGG CTTGTCTGACCTGAGGAGGTGGCTG
7478	Table 3A	NA	AA501725	2236692	ng18e12.s1 NCI_CGAP_Lip2 cDNA clone IMAGE:929806 similar to contains Alu repetitive element, mRNA	-1	AACTCCATAGAGAAAGACTACGAATT TCGCTGGGAGGTAAATAGGGAGCC
7479	Table 3A	NA	AA501934	2236901	nh56a10.s1 NCI_CGAP_Pr8 cDNA clone IMAGE:956346, mRNA sequence	-1	GCATTTAGGAAAGACAGGTGAGTGTG CCACAACCTAACACATCAGCA
7480	Table 3A	NA	AA579400	2357584	nf33d05.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:915561 similar to contains Alu repetitive element;contains	-1	TTACTTTGTCTCTCACCATCTAA AACGTTGTTGCTGAGCATGAA
7481	Table 3A	NA	AF249845	8099620	Isolate Siddi 10 hypervariable region I, mitochondrial sequence	-1	CCCCAGACGAAAATACCAAATGCATG GAGAGCTCCCGTGAGTGGTTAATA
7482	db mining	Hs.277051	AI630242	4681572	ad07c09.y1 cDNA /clone=ad07c09- (random)	-1	GCCTAAGTTCCAGAACAGTTTGACG ATGGAGAGCATGCAAACGAGGTAA
7483	db mining	Hs.277052	AI630342	4681672	ad08g11.y1 cDNA /clone=ad08g11- (random)	-1	TTTGCAGTTCAAGGATTGGTGGGAA ACGTTTGTATGTGTTGGGGTGGG

Table 8

7484	db mining	NA	AI732228	5053341	nf19e05.x5 NCI_CGAP_Pr1 cDNA clone IMAGE:914240 similar to contains Alu repetitive element; mRNA s	-1	AATAGATTCATTTCTCCCTCGAGTAGTTGGTATTGGACCTGAA
7485	Table 3A	Hs.197803	AW379049	6883708	mRNA for KIAA0160 gene, partial cds /cds=(0,2413)	-1	CGACGGTGTCTGGAGTTCGATGAGACATGTAAGTAAGAGTCTGTGCA
7486	Table 3A	Hs.232000	AW380881	6885540	UI-H-BloP-abh-h-06-0-Uls1 cDNA, 3' end /clone=IMAGE:2712035 /clone_end=3'	-1	ATATTCAAGCAGTGGCTGTGAAATTGGATTGAAATTACCGGGATACATGCA
7487	Table 3A	Hs.325568	AW384988	6889647	602386081F1 cDNA, 5' end /clone=IMAGE:4514972 /clone_end=5'	-1	ACTGGTTTCTTCTAGTGTCCCCCACCGTCTAGTTCTATTCTGTGA
7488	Table 3A	NA	AW836389	7930363	PM0-LT0030-101299-001-f08 LT0030 cDNA, mRNA sequence	-1	TTGGGAGTCACCCAGGTTAAAGCAAAG CCTCAGTCAGTAAAGCAGAAACT
7489	Table 3A	NA	AW837717	7931691	CM2-LT0042-281299-062-e11 LT0042 cDNA, mRNA sequence	-1	TCTCTGTGCTCCAGAATTAGTGTGATTGC TTGGTGTCTTAACCTGAAAGTGGGA
7490	Table 3A	NA	AW837808	7931782	CM1-LT0042-100300-140-f05 LT0042 cDNA, mRNA sequence	-1	CATCTGCTCTGCTTCTCACACACTA GAAACACCACTGCCCCCATCCATG
7491	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence	-1	TCTGTGATTTATAGTGTGTTAGGA AACGATCTTCCCATCTGTGGTGA
7492	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	-1	TCATTCAGGCTTAATAAAACACACTAA CCTCGGCGAGCAGTGGAGCGCTG
7493	Table 3A	NA	AW856490	7952183	PM4-CT0290-271099-001-c04 CT0290 cDNA, mRNA sequence	-1	AGCTTAGGATATCTATTAGTGTCACT GTTGGGCAAGAGGCCAAAGGG
7494	Table 3A	NA	AW891344	8055549	PM2-NT0079-030500-001-a04 NT0079 cDNA, mRNA sequence	-1	TGGGAACACACTGGGCCCATTATATAG AGAAAATAAACATGATCCCCAT
7495	Table 3A	NA	BE061115	8405765	QV0-BT0041-011199-039-f09 BT0041 cDNA, mRNA sequence	-1	TTGCTTGATTTCCCAAACCACTACCT GAAGGTGCGTTATGGTCTACAGCT
7496	Table 3A	NA	BE086076	8476469	PM2-BT0672-130400-006-h09 BT0672 cDNA, mRNA sequence	-1	TTCCACCACTTCAAGACTGGGGGCA GGTAGAGAAAGACAAGCATAAGTACA
7497	Table 3A	NA	BE091932	8482384	IL2-BT0733-130400-068-C11 BT0733 cDNA, mRNA sequence	-1	TTCTCTGCTTCCACACCCCTCC CTCACATCTGGTTACAAGTTG
7498	Table 3A	Hs.173334	BE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922)	-1	CAGCACATCTGGTTACAAGTTG GTAACTATGAAAGCTGGAGATGC
7499	Table 3A	NA	BE163106	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence	-1	TATCTAAATTCTACCTTAGCATCCAA CTAGCTACCGTCTGGCACTGGC
7500	Table 3A	Hs.301497	BE168334	8631159	arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544)	-1	TCCAATGCTCAAGTCACTCTGAGTCT TTGCTGGTGTCAACCTACAATGCC
7501	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453468 /clone_end=5'	-1	ACCTCACTATAGTAGCCATTAGGTA AGATGGCCATATCAAATGGCT
7502	Table 3A	NA	BE177681	8655813	RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence	-1	AAGAACTATTCCTTGGAGAACATTTCC TACTGGGAGTTACTGCTGTGATT
7503	Table 3A	NA	BE178880	86558032	PM1-HT0609-060300-001-g03 HT0609 cDNA, mRNA sequence	-1	TCTGTGTGAACATACATACAGGACTT TGATTCTACCTGTGCTGACCATT
7504	Table 3A	Hs.865453	BE247058	9098807	602495247F1 cDNA, 5' end /clone=IMAGE:4609330 /clone_end=5'	-1	GTGGAGCTGTGGCTTGGCTGGATG CGGGCACTCTCACACCTTCAGGTA
7505	Table 3A	Hs.11050	BE763412	10193336	mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	-1	TGTCAGTGGCTCTCACTTTGTTGAA ATTGTTGCTTGGGAAAAACACAG
7506	Table 3A	NA	BF330908	11301658	RC3-BT0333-310800-115-f11 BT0333 cDNA, mRNA sequence	-1	GATGCAGTGGGTTAGGGTTGGGG TACAGACTGACTGAGCTGGAGTC
7507	Table 3A	NA	BF357523	11316597	CM2-HT0945-150900-379-g06 HT0945 cDNA, mRNA sequence	-1	TCAGGCACTCAGTAAGGCAAGACT GAGTGTACATAAAGTCAGTTACA
7508	Table 3A	NA	BF364413	11326438	RC6-NN1068-0670600-011-B01 NN1068 cDNA, mRNA sequence	-1	CCTTGGGCTGAGTTGCTGGCTGTA AGATTACAGTTGGTTAGAGAGA
7509	Table 3A	NA	BF373638	11335663	MRO-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	-1	ACAGCAACAAAGTGTCCAATCCCTC TATTAACCCATTAAACCAAGAGTT
7510	Table 3A	NA	BF740663	12067339	QV1-HB0031-071200-562-h04 HB0031 cDNA, mRNA sequence	-1	AGTGCATTTCACAGGTTGCTTCT TAGTAGCTTCACAGGTTGCTT
7511	Table 3A	NA	BF749089	12075765	MR2-BN0368-051000-014-b04 BN0386 cDNA, mRNA sequence	-1	AAAGTGTGATTAGAAGCAGCTGGAAAGT AGCAGAGGAGGTGGAAGTTAGTCC
7512	Table 3A	NA	BF758480	12106380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	-1	CAGGAGTAAACAGAGCTGGTTGTG TATAACCTATGCTGGGTGGAAGACT
7513	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	-1	GGTGAECTATCTTACCGGCTCCAGTA AACTCTGAACAAATGTACCGCTAA
7514	Table 3A	NA	BF773393	12121293	CM2-IT0039-191200-638-h02 IT0039 cDNA, mRNA sequence	-1	GCTTGAAGATGTCTAACAGAAAATC ACCGACATGAGGAAGCATCACGCT
7515	Table 3A	NA	BF805164	12134153	QV1-CI0173-081100-456-f03 CI0173 cDNA, mRNA sequence	-1	TCTAGGGCAGGAACATGGCTGCAGC ATATAAAAAGAATTGAATTCCATACTT TTGT
7516	Table 3A	NA	BF818594	12156027	MR3-CI0184-201200-009-a04 CI0184 cDNA, mRNA sequence	-1	GGTGCCTGCCATAGGTGCCAGTAATG ACCGTTTATGCGGAATCAATTACA
7517	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08 HN0025 cDNA, mRNA sequence	-1	TGAAGTACTATAGGACTCAATGGGAC CAGTAGCAGCTCCAACTGGATCAC
7518	Table 3A	NA	BF845167	12201450	RC5-HT1035-271200-12-F08 HT1035 cDNA, mRNA sequence	-1	ACACGGGACCTCCCTTGTATCTCTG AGAATTAATAGAGATTATGCA

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7519	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119 cDNA, mRNA sequence	-1	CCAAAAGGAGAAAGATGACTAGGGT CACACTTGGGATTGCCAGGTGGG
7520	Table 3A	NA	BF875575	12265705	QV3-ET0100-111100-391-c02 ET0100 cDNA, mRNA sequence	-1	GCATCTTCTTGAAAGACGGGAACGT ACTTCAGGTCTTTCTGTTAGC
7521	Table 3A	NA	BF877979	12268109	MRO-ET0109-171100-001-b02 ET0109 cDNA, mRNA sequence	-1	GGCTCATTTGGTTTAAAGTCTTCT ATGCCATCCCAGGGGAGGGAGAT
7522	Table 3A	NA	BF897042	12288501	IL2-MT0179-271100-254-C11 MT0179 cDNA, mRNA sequence	-1	GACTGTGGACACCTCTCACTGTGCT TCTGGCAGGAGCTACTGAC
7523	Table 3A	NA	BF898285	12289744	QV1-MT0229-281100-508-e11 MT0229 cDNA, mRNA sequence	-1	GCAGGGTGCAGAGCTTCACAGCAGG TAGGAAAGTAACATAAGTGGAAC
7524	Table 3A	NA	BF899464	12290923	IL5-MT0211-011200-317-f03 MT0211- cDNA, mRNA sequence	-1	CAGCTAAAGCCGTAGGTCTATTGTGAC TGTCCCTGGGATGTGGATTACTCT
7525	Table 3A	Hs.324473	BF904425	12295884	40 kDa protein kinase related to rat ERK2 /cds=(134,1180)	-1	CCAAATGCAAGCTACAGACCAAATA TCAATGGACTGGTAGGCCCTGC
7526	Table 3A	NA	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	-1	TTAAACCAGGTCTGGAAAAAGGAAG GAGGGAGGGCATTTAGAGAAGA
7527	Table 3A	Hs.104679	BF926187	12323197	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds /cds=(2206,2373)	-1	GTGGCTCGAAATAGAAGAGCACT CACTGTGGAACATACAAATGGCGA
7528	Table 3A	Hs.75703	BF928644	12326772	small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386)	-1	CACACCACAGCTGGCTGGGAGCAGA GGCTGCTGGTCTCATAGTAATCTAC
7529	Table 3A	NA	BG006820	12450386	RC4-GN0227-271100-011-d03 GN0227 cDNA, mRNA sequence	-1	TGGAGAAAATGAGAGACAGACAGTG AGTGAGAAAGTCAGCGAAAGGAAA
7530	Table 3A	NA	F11941	706260	HSC3F051 normalized infant brain cDNA cDNA clone c-33f05, mRNA sequence	-1	ACCTACTGTTGAGATTATCCCCCTGT CTCCACACTGCCAGAACTTACCA
7531	Table 3A	NA	U46388	1236904	HSU46388 Human pancreatic cancer cell line Patu 8988t cDNA clone xs425, mRNA sequence	-1	CCAAATGATACTAGGATTAAGCCCCA AAGCAAAGTCAAAGCACCACCATGG
7532	Table 3A	NA	U75805	1938265	HSU75805 Human cDNA clone f46, mRNA sequence	-1	TCCCAGAGCAACAACTAAGTCTAAC TAATGGACACCAACACCCACTGA
7533	Table 3A	NA	W27656	1307658	36f10 Human retina cDNA randomly primed sublibrary cDNA, mRNA sequence	-1	CCACAGAATGGGCATGTAGTATTGAG ATTGAAATCATCTGCTGTCCAGCC
7534	literature	Hs.99962	BC005929	13543541	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein) (PRG2), mRNA /cds=(857,1525)	1	TACTGGCGTCGAGGCCACTGCCTCA GAAGACTTCCTTCATCTGTTCTA
7535	literature	Hs.46295	X14346	31182	eosinophil peroxidase (EPX), mRNA /cds=(0,2147)	1	GTTCAAGGGACATCTCAGAGCCAA CATCTACCTCGGGGCTTGTGAA
7536	literature	Hs.1256	J05225	179076	arylsulfatase B (ARSB), mRNA /cds=(559,2160)	1	CTACAGTTCTACCATAAACACTCAGT CCCGTGTACTTCCCTGACAGGA
7537	literature	Hs.728	M28129	556208	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA /cds=(71,556)	1	TAGTTGCATGTGACAACAGAGATCAA CGACGAGACCCCTCACAGTATCCG
7538	literature	Hs.889	NM_001828	6325464	Charcot-Leyden crystal protein (CLC), mRNA /cds=(33,461)	1	TTGACCATAGAACATAGGCCTGAGGCT GTGAAGATGGTCAAGTGTGGAGA
7539	literature	Hs.135826	M89138	180539	chymase 1, mast cell (CMA1), mRNA /cds=(0,743)	1	CTGCTGTCTCACCCGAATCTCCCAT TACCGCCCTGGATCAACCAGATC
7540	literature	Hs.334455	NM_003293	13699841	tryptase, alpha (TPS1), mRNA /cds=(17,844)	1	GTCACTGGAGGAACCAACCCCTGCTG TCCAAAACACCAACTGCTTCTTACCC
7541	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	CATGCCATGCATATTCAACTGGCT GTCTATTTCGACACCAGCTTATT
7542	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	GAGAACGACCTAACCTGGAGACAAT TCTACTGTTCAAACAGCAGCAGCA
7543	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	ACTTGTCAGGGCATTCTCTCCGG GCACTGGGTCACTAGGACTGTTT
7544	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	GACAGCGCTCCATAAAACCTGGCGA, CCATTGCTCCAGCGGGATAGAGTG
7545	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	CATCTCTGGACCCCTGACCTGTGATC GTGCGCATCATAGACCAGCCAGTAGA
7546	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	GCCTCACACGACATCACACCATATA CCGCAAGGAATATCAGGGATCTG
7547	literature	Hs.279852	BC004555	13528716	G protein-coupled receptor (G2A), mRNA /cds=(900,2042)	1	ACAGCCATCCTCCCTTGAGAGTCAT CAGAAAAATACATTAGAAAATGT
7548	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	ACCTTCGTCTCTGAGTCATGCCT CAAAACCTAGTTTGTAGACAGGAA
7549	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	AGATGGCTACCCCTCTGATTATGATC CTTTCGTAGAAAATGCTCAAATCT
7550	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	ATGCATCGCCGACAAGTCTGAAATT GGATTTGTCGAAATTAGACAAAGAA
7551	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	CGGGTGTGTTCAATCATCGACGGTGA CAATCCTATCTCATCTATAATCC
7552	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	GAAGAGCGAAATGCAATCTCTGCTT CTTCAGTAGAGACTTACAGTCTT
7553	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	GCACATCCATCGCCCAAAGTGAAGTC TGAAGGATGCATTTTGGTTG
7554	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	TCTCGGTTACCTTTGCTGTGTTG GTTCTTGTCTTGCTGGTTGCT

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7555	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	TCTGAATACTCTACAAAACGCTCCCTT
7556	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	GTCGCTCTAAACCATCTGTGT
7557	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	TGAAGCTGACACCTGTGAAACTAAGT
7558	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	TAACCGCATGTTCTTGACTCAG
7559	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	TTCTGTTTGGGCCAGGAACCGTTCT
7560	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	ATAAAATTGTTTATTGACTACACG
7561	literature	NA	NC_001664	9628290	Human herpesvirus 6, complete genome	1	TAACACCGTCCAAGAAATTGCGGT
7562	db mining	Hs.159568	AI382620	4195401	qz04e10.x1 cDNA, 3' end /clone=IMAGE:2020554 /clone_end=3'	1	TGTTGCCCCATACCTCTTAGGGC
7563	db mining	Hs.129055	NM_002540	4505490	Homo sapiens, Similar to outer dense fiber of sperm tails 2, clone MGC:9034 IMAGE:3874501, mRNA, complete cds /cds=(656,2947)	1	AGAAGAAGGATCAGATGGAGAGTTG
7564	db mining	Hs.12329	AB014597	3327207	mRNA for KIAA0697 protein, partial cds /cds=(0,2906)	1	AAAACCTTAACTGGTAAGTACATGA
7565	db mining	Hs.119177	NM_001659	4502202	ADP-ribosylation factor 3 (ARF3), mRNA /cds=(311,856)	1	CCGATACCGGCAAGATCTGCGTCTG
7566	db mining	Hs.12379	BC003378	13097227	Homo sapiens, LWS (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R), clone MGC:5084 IMAGE:2901220, mRNA, complete cds /cds=(142,1122)	1	GCAAACCTGTTCCACCTTATGTT
7567	db mining	Hs.319886	AL589290	13243062	DKFZp451F1715_r1 cDNA, 5' end /clone=DKFZp451F1715 /clone_end=5'	1	ACTACATTITAATAAAGATAATGGG
7568	db mining	Hs.315597	NM_015960	7705727	cDNA FLJ10280 fis, clone HEMBB1001288, highly similar to CGI-32 protein mRNA /cds=UNKNOWN	1	CATATTAGAAGTTCTCAAAGTTC
7569	db mining	Hs.110457	AF071594	3249714	MMSET type I (WHSC1) mRNA, complete cds /cds=(29,1972)	1	AAAAGGAGTGAAGCTATCATCAGTGT
7570	db mining	Hs.144904	NM_006311	5454137	nuclear receptor co-repressor 1 (NCOR1), mRNA /cds=(240,7562)	1	GTGAACTTAAACGCGATGACTGTG
7571	db mining	Hs.118064	NM_022731	12232386	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(66,557)	1	ACACAGAACATTGAGCATTGTAT
7572	db mining	Hs.337616	NM_000753	4502924	phosphodiesterase 3B, cGMP-inhibited (PDE3B), mRNA /cds=(0,3338)	1	TTCTCGCATCCCTCTCGTGAACGG
7573	db mining	Hs.152049	AW962287	8152099	EST374360 cDNA	1	ACAGACTTGGTATGAATTAGAGTGT
7574	db mining	Hs.115325	NM_003929	4506374	RAB7, member RAS oncogene family-like 1 (RAB7L1), mRNA /cds=(40,651)	1	GACTTAAGGGTCAATTCAAAGCAG
7575	db mining	Hs.119178	AK024466	10440445	mRNA for FLJ00059 protein, partial cds /cds=(2624,4057)	1	ACAGACTTGGTATGAATTAGAGTGT
7576	db mining	Hs.183698	NM_000269	4557798	ribosomal protein L29 (RPL29), mRNA /cds=(29,508)	1	TTCTTATTTCTAACTCTGCTGAC
7577	db mining	Hs.15767	AB023166	4589541	mRNA for KIAA0949 protein, partial cds /cds=(0,2822)	1	ACTTCATCATATAATTGGAGGGAAAGCT
7578	db mining	Hs.108104	NM_003347	4507788	ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA /cds=(15,479)	1	CTTGGAGCTGTGAGTTCTCCCTG
7579	db mining	Hs.183593	NM_000980	11415025	ribosomal protein L18a (RPL18A), mRNA /cds=(19,549)	1	AGAACGAGGAAGAGAACACAAGGAA
7580	db mining	Hs.121044	L39061	632997	transcription factor SL1 mRNA, partial cds /cds=(0,1670)	1	TGATTCAAGATCCACCTTGAGAGGA
7581	db mining	Hs.309348	NM_032472	14277125	tc93c11.x1 cDNA, 3' end /clone=IMAGE:2073716 /clone_end=3'	1	AGAGAATAGGCTTCTAAGATGCTGC
7582	db mining	Hs.16493	AK027866	14042851	cDNA FLJ14960 fis, clone PLACE4000192, weakly similar to ZINC FINGER PROTEIN 142 /cds=(114,3659)	1	GATCCCGTTCTGCTGCCGTAAATA
7583	db mining	Hs.1342	NM_001862	4502982	cytochrome c oxidase subunit Vb (COX5B), nuclear gene encoding mitochondrial protein, mRNA /cds=(21,410)	1	AGGCAACACCCCTTCTAGGTG
7584	db mining	Hs.111076	NM_005918	5174540	malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(86,1102)	1	AGGCAACTACTGCTGACTAAGAATT
7585	db mining	Hs.107476	NM_008476	5453560	ATP synthase, H+ transporting, mitochondrial F1Fo, subunit g (ATP5JG), mRNA /cds=(73,384)	1	AGGGAGAATCTGTATACTTGCTGG

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7586	db mining	Hs.146354	NM_005809	5902725	peroxiredoxin 2 (PRDX2), mRNA /cds=(89,685)	1	CAAGCCCACCCAGCCGCACACAGGC
7587	db mining	Hs.12124	NM_018127	11875212	elaC (<i>E. coli</i>) homolog 2 (ELAC2), mRNA /cds=(0,2480)	1	CACCGAGACAAGCAGAGTAACAGG
7588	db mining	Hs.154023	AB011145	3043669	mRNA for KIAA0573 protein, partial cds /cds=(0,1356)	1	CAGGAGGTAGGGATCTGGCTGAGAG
7589	db mining	Hs.109051	NM_031286	13775197	SH3BGRl3-like protein (SH3BGRl3), mRNA /cds=(71,352)	1	GAGTCCCTCTCCAGGAGGACCTA
7590	db mining	Hs.125307	AA836204	2910523	od22g11.s1 cDNA /clone=IMAGE:1368740	1	GAGGCAATTAAATGATGCTGTTTC
7591	db mining	Hs.16803	NM_018032	8922296	LUC7 (<i>S. cerevisiae</i>)-like (LUC7L), mRNA /cds=(71,1048)	1	CATGAGAAGTATCTGCAATAACCCCA
7592	db mining	Hs.146580	NM_001975	5803010	enolase 2, (gamma, neuronal) (ENO2), mRNA /cds=(222,1526)	1	AGTCAACATTAGGTTTGTCACA
7593	db mining	Hs.14169	AK027567	14042333	cDNA FLJ14661 fis, clone NT2RP2002710, weakly similar to SH3-BINDING PROTEIN 3BP-1 /cds=(70,2481)	1	CCATGCCGCCTGTTGGATTGTCGG
7594	db mining	Hs.118625	NM_000188	4504390	hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein, mRNA /cds=(81,2834)	1	AATGTAGACAGAAATGTACTGTTCT
7595	db mining	Hs.144505	NM_015653	13124762	DKFZP566F0546 protein (DKFZP566F0546), mRNA /cds=(377,1306)	1	CCCACGGGAGACTATTTCACACAATT
7596	db mining	Hs.155751	NM_004889	4757811	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit f, isoform 2 (ATP5J2), mRNA /cds=(27,311)	1	TAATACAGGAAGTCGATAATGAGG
7597	db mining	Hs.10267	NM_015367	7662505	MIL1 protein (MIL1), nuclear gene encoding mitochondrial protein, mRNA /cds=(71,1231)	1	CCCTCCGTGAGGAACACAATCTCAAT
7598	db mining	Hs.14632	BC008013	14124973	Homo sapiens, Similar to CG12113 gene product, clone IMAGE:3532726, mRNA, partial cds /cds=(0,2372)	1	CGGTGTCTTCCAGCCCTAAAGGAAG
7599	db mining	Hs.125156	NM_001488	4503956	transcriptional adaptor 2 (ADA2, yeast, homolog)-like (TADA2L), mRNA /cds=(0,1091)	1	GGCAGACCCGTCTTTCCATGCC
7600	db mining	Hs.159545	NM_013308	7019400	platelet activating receptor homolog (H983), mRNA /cds=(219,1178)	1	CCCTCAAAGGTCACTGAGACTTTGC
7601	db mining	Hs.152936	NM_004068	4757993	adaptor-related protein complex 2, mu 1 subunit (AP2M1), mRNA /cds=(135,1442)	1	CTCACCTAAAGAGACCAAGGCTCA
7602	db mining	Hs.110857	NM_016310	7706498	polymerase (RNA) II (DNA directed) polypeptide K (12.3 kDa) (POLR3K), mRNA /cds=(39,365)	1	CGGCCTCAGTCCCTACTCTGCTTTGG
7603	db mining	Hs.118666	NM_025207	13376805	hypothetical protein PP591 (PP591), mRNA /cds=(820,1704)	1	GATAGTGTGAGCTTACGGCAGTAT
7604	db mining	Hs.16390	AK024453	10440419	mRNA for FLJ0045 protein, partial cds /cds=(106,924)	1	CTTTCAGATCCCTCTGGTCTCCGTC
7605	db mining	Hs.109302	AA808018	2877424	nv64d09.s1 cDNA, 3' end /clone=IMAGE:1234577 /clone_end=3'	1	CGAAATTACAGGCCAGGGCACTCTT
7606	db mining	Hs.111126	NM_004339	11038670	pituitary tumor-transforming 1 interacting protein (PTTG1IP), mRNA /cds=(210,752)	1	TTTTTATTTCATTATGTGGCCA
7607	db mining	Hs.127376	NM_021645	11063982	KIAA0266 gene product (KIAA0266), mRNA /cds=(733,3033)	1	GACTCCCTCAACACCCCAAACCTCTA
7608	db mining	Hs.108196	NM_016095	7706366	HSPC037 protein (LOC51659), mRNA /cds=(78,635)	1	AATGCCACGGTCATCTGTTCTAT
7609	db mining	Hs.117487	AF040965	2792385	unknown protein IT12 mRNA, partial cds /cds=(0,2622)	1	GAGCAGCCACAAAAACTGTAACCTAA
7610	db mining	Hs.107882	NM_018171	8922576	hypothetical protein FLJ10659 (FLJ10659), mRNA /cds=(38,1000)	1	GGAAACCATAAACGCTTGGAGTGC
7611	db mining	Hs.147585	NM_024785	13376147	hypothetical protein FLJ22746 (FLJ22746), mRNA /cds=(266,1072)	1	GCAGCAAACAGAGGGTCAGTCACAG
7612	db mining	Hs.153357	NM_001084	4505890	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 (PLOD3), mRNA /cds=(216,2432)	1	GATGTTCTGCTTGGCATCAACCAA
7613	db mining	Hs.148495	NM_002810	5292160	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 (PSMD4), mRNA /cds=(62,1195)	1	GGCGTACAGCTTGTGCTTGGCATAACAA
7614	db mining	Hs.13144	NM_014182	7661819	HSPC160 protein (HSPC160), mRNA /cds=(53,514)	1	GGGGTTCTGCTTGGCATCAACAA
7615	db mining	Hs.1189	NM_001949	12669913	E2F transcription factor 3 (E2F3), mRNA, complete cds /cds=(66,1463)	1	ATACTGAGGGATGGGTTGGGAC
7616	db mining	Hs.12284	BC001699	12804564	Homo sapiens, clone IMAGE:2989556, mRNA, partial cds /cds=(0,370)	1	GGGTGACCTGTTCTAGCTGTGATC

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7617	db mining	Hs.158380	AI381581	4194362	td05e04.x1 cDNA, 3' end /clone=IMAGE:2074782 /clone_end=3'	1	GTACCACTTGAATGATTTCAGTCATT TTGAACCCCTTGGAAAGAGGTG
7618	db mining	Hs.1390	BC000268	12653014	Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 2, clone MGC:1664 IMAGE:3352313, mRNA, complete cds /cds=(58,663)	1	GTGAAACCCCGTCTCTGCTAAAAATA CAAAAATTAGCTGGCGTGGTGGC
7619	db mining	Hs.115808	NM_002287	11231175	leukocyte-associated Ig-like receptor 1 (LAIR1), transcript variant a, mRNA /cds=(57,920)	1	GTTCTCTGGGTTGTGCTTACTCCAC GCATCAATAATAATTGAAGGC
7620	db mining	Hs.119960	AL117477	5911950	mRNA; cDNA DKFZp727G051 (from clone DKFZp727G051); partial cds /cds=(0,1423)	1	TACTGCCAAC TGACCTTATAAACCTC TGCACCTCAAAAGATTCATGGT
7621	db mining	Hs.154073	NM_005827	5032212	UDP-galactose transporter related (UGTREL1), mRNA /cds=(87,1055)	1	TCAAACAGTGACATCTTGGAAAAA TTGACTTAATAGGAATATGGACT
7622	db mining	Hs.11747	NM_017798	8923363	hypothetical protein FLJ20391 (FLJ20391), mRNA /cds=(9,602)	1	TCACTCCCTGAACCTGTACTGCCT GAATGGAGTCCTGGACGACATTGG
7623	db mining	Hs.10881	AB011113	3043605	mRNA for KIAA0541 protein, partial cds /cds=(0,3484)	1	TCCACTTAATAGACTCTATGTGCT GAATGTTCCCTGTGACATATGTGT
7624	db mining	Hs.153850	AK024476	10440465	mRNA for FLJ0069 protein, partial cds /cds=(2657,4396)	1	TCCCGCAGAGTGCAGAGACAGGAAG CTGGAGATGTCTTTATAAAGTCACA
7625	db mining	Hs.247870	AL035694	4678462	DNA sequence from clone 33L1 on chromosome 6q14.1-15. Contains the gene for novel T-box (Brachyury) family protein. Contains ESTs, STSs, GSSs and two putative CpG Islands /cds=(0,1505)	1	TCTAGGACCTAGGAAGCTTAAC TGTACATCTCAAGTATCTGCACA
7626	db mining	Hs.324848	NM_003128	4507194	cDNA FLJ13700 fis, clone PLACE2000216, highly similar to SPECTRIN BETA CHAIN, BRAIN /cds=UNKNOWN	1	TCTCCGCCATCTCTCTGATAAACAC CGAGGTGTCTGCCAGCACCCAGAG
7627	db mining	Hs.118722	NM_004480	4758407	fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA /cds=(716,2443)	1	TGATATGTTGATCAGCCTTATGTGGA AGAACTGTGATAAAAGAGGAGCT
7628	db mining	NA	AL134726	6602913	DKFZp547A1290_r1 cDNA, 5' end /clone=DKFZp547A1290 /clone_end=5'	1	TGAGTATTTCAAACCTCTGGTCG CAAACCCATTAGTAGTTGTGAAA
7629	db mining	Hs.166887	NM_003915	4503012	copine I (CPNE1), mRNA /cds=(156,1769)	1	TGCTGCTCTGATCCCACCTTGTGTC CTGACAACCCCTCATCAATAAGA
7630	db mining	Hs.146324	AK023182	10434993	cDNA FLJ13120 fis, clone NT2RP3002682, highly similar to CGI-145 protein mRNA /cds=(176,961)	1	TGGTTTGTICATGGATGTATTCTAAG AGCTGAGAACAGGGCCTGGACACA
7631	db mining	Hs.12436	AK026309	10439130	cDNA: FLJ22656 fis, clone HSI07655 /cds=UNKNOWN	1	TGTTCTGAATGTTGGTAGACCCCTCA TAGCTTGTATCAAATGAAACCTTG
7632	db mining	Hs.15164	NM_006333	5453582	nuclear DNA-binding protein (C1D), mRNA /cds=(117,542)	1	TGTTGATGGATGAAATTGGCATGAT GACTGTACTCTCAATAAAGGCTGA
7633	db mining	Hs.130743	AA642459	2567677	ns30d01.s1 cDNA, 3' end /clone=IMAGE:1185121 /clone_end=3'	1	TTCATCTGTGAGTGCTGGGGAGGA GGAGTAGATACAGACTGAGTGAGAG
7634	db mining	Hs.16492	NM_015497	13794264	DKFZP564G2022 protein (DKFZP564G2022), mRNA /cds=(42,1709)	1	TTCATTTCTGGGAAGTCAGGGTTTTGAGA CATCTTGAGAGGTTGTTTGAGA
7635	db mining	Hs.122552	NM_016428	7705281	G-2 and S-phase expressed 1 (GTSE1), mRNA /cds=(70,2232)	1	TTCTAAGCCGAACCAAATCCTTGCCT TTGAAAGAACAGCCCCTAAAGTGGT
7636	db mining	Hs.312610	AI174807	6361196	HA2528 cDNA	1	TTTGTGTTTGTTCAGATAGGTCT CCCTCTGTACCCAGGCTGCAGT
7637	db mining	Hs.108258	NM_012090	10048480	actin cross-linking factor (ACF7), transcript variant 1, mRNA /cds=(51,16343)	1	TTTTGTAATCACGGACACCTCAATT A GCAAGAACTGAGGGAGGGCTT
7638	db mining	Hs.111092	NM_024724	13376033	hypothetical protein FLJ22332 (FLJ22332), mRNA /cds=(275,1255)	1	CGGTGTGGAAAATGTTGCTTTGAG TGGCAAGAATTAGAAAAATCTCA
7639	db mining	Hs.114311	NM_003504	4502712	CDC45 (cell division cycle 45, <i>S.cerevisiae</i> , homolog)-like (CDC45L), mRNA /cds=(24,1724)	1	CTGAAAGCTGAGGATCGGAGCAAGT TTCTGGACGCACCTATTCCCTCCT
7640	db mining	Hs.11081	NM_025241	13376853	UBX domain-containing gene 1 (UBXD1), mRNA /cds=(96,1421)	1	GTGCCCCCTCAGCCCTGTGGGTCTGT CTCATGCTCTCCCTGTTCCCTCC
7641	db mining	Hs.100217	NM_005892	5174400	formin-like (FMNL), mRNA /cds=(39,1430)	1	TAGCCATACCTAGCCTCAGCAGGAGC CTGGCCCTGTAACTTATAAAGTGCA
7642	db mining	Hs.12258	AL137728	6808258	mRNA; cDNA DKFZp434B0920 (from clone DKFZp434B0920) /cds=UNKNOWN	1	TGAGGGCTGTGCTGACCTTTGAGAG GATTGAAATTGCTTCATATTGTGA
7643	db mining	Hs.155462	NM_005915	7427518	minichromosome maintenance deficient (mis5, <i>S. pombe</i>) 6 (MCM6), mRNA /cds=(61,2526)	1	TGTGTAAGAAAAGGCCATTACTTTT AAGGTATGTGCTGTCTATTGAGC
7644	db mining	Hs.165998	NM_015640	7661625	PAI-1 mRNA-binding protein (PAI-RBP1), mRNA /cds=(85,1248)	1	TTGTTGGTAGGCACATCGTGTCAAGT GAAGTAGTTTATAGGTATGGTT
7645	db mining	Hs.164207	NM_024805	13376184	hypothetical protein FLJ21172 (FLJ21172), mRNA /cds=(138,1169)	1	TTCTAGCTTCCGTGTATCTAAACA CAATTGCTACACAAAGTCACTGT
7646	db mining	Hs.150275	D87682	1663699	mRNA for KIAA0241 gene, partial cds /cds=(0,1568)	1	ACTGTGGCACATGTTTGTAGCAGAAA GGTAGTTCTTGTCTGGTAGT

Table 8

7647	db mining	Hs.11039	NM_024102	13129109	hypothetical protein MGC2722 (MGC2722), mRNA /cds=(69,1097)	1	CATCTCTGCCCTGGTCCCCTTC
7648	db mining	Hs.102708	NM_015396	7661561	DKFZP434A043 protein (DKFZP434A043), mRNA /cds=(697,1425)	1	TTGATGTGAAAGTCTGAATGCAG
7649	db mining	Hs.109546	NM_002493	4505364	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17) (NDUFB6), mRNA /cds=(68,454)	1	CGCTCTAACATGCATTCTGTTCTC
7650	db mining	Hs.142307	AL137273	6807710	mRNA; cDNA DKFZp434l0714 (from clone DKFZp434l0714) /cds=(0,412)	1	CTTTTGCCCTGATTGTAATCCA
7651	db mining	Hs.16297	NM_005694	5031644	COX17 (yeast) homolog, cytochrome c oxidase assembly protein (COX17), mRNA /cds=(86,277)	1	CTGGAGACTGGAGAAGTAATTCACC
7652	db mining	Hs.11184	NM_017811	8923387	hypothetical protein FLJ20419 (FLJ20419), mRNA /cds=(191,907)	1	AATGAAAAGAATTCCCTGATCAACA
7653	db mining	Hs.12013	NM_002940	4506558	ATP-binding cassette, sub-family E (OABP), member 1 (ABCE1), mRNA /cds=(117,1916)	1	TCAGTGTTTCTGTTATTCCATATCAGTG
7654	db mining	Hs.155485	NM_005339	12545382	huntingtin interacting protein 2 (HIP2), mRNA /cds=(77,679)	1	GCTTTTACTGTCAAAGATTGTGT
7655	db mining	Hs.154573	AW955094	8144777	EST367164 cDNA	1	TGCATGAGAGCCCTAGGATTTAAAT
7656	db mining	Hs.142157	AF080255	5733121	lodestar protein mRNA, complete cds /cds=(30,3518)	1	ATGAAATGCTCCCTTATTACCTCCCA
7657	db mining	Hs.1191	AK025679	10438273	cDNA: FLJ22026 fis, clone HEP08537 /cds=UNKNOWN	1	AAGGTACCGAGCCTTGAATTAA
7658	db mining	Hs.13340	NM_003642	4504340	histone acetyltransferase 1 (HAT1), mRNA /cds=(36,1295)	1	ACACACTAATGTAACCATTTATGAAG
7659	db mining	Hs.108110	NM_014034	7661591	DKFZP547E2110 protein (DKFZP547E2110), mRNA /cds=(192,806)	1	GTGAGACTGGGAGTGGCGAGA
7660	db mining	Hs.123295	AA833793	2908561	od61g07.s1 cDNA /clone=IMAGE:1372476	1	GTGGATGAGTAGGGAGTGGCGAGA
7661	db mining	Hs.126565	AB020668	4240210	mRNA for KIAA0861 protein, partial cds /cds=(0,2948)	1	TTGGATGTGTTAGTGCAAGATTGC
7662	db mining	Hs.155174	AB007892	2887434	KIAA0432 mRNA, complete cds /cds=(2251)	1	TTCTGTGAGATTCCTCGCATTTC
7663	db mining	Hs.116445	AA648776	2575205	ns24d11.s1 cDNA, 3' end /clone=IMAGE:1184565 /clone_end=3'	1	ACTAGAGTCCAGTAATAGTAGTGGA
7664	db mining	Hs.124933	AA825303	2898605	oc67e04.s1 cDNA, 3' end /clone=IMAGE:1354782 /clone_end=3'	1	GGCTGTTGAGATGGAGACATGATAGGT
7665	db mining	Hs.313267	AW295641	6702277	UI-H-BW0-aip-e-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729975 /clone_end=3'	1	TATACCTGAATACTTTATGACAACCTGAG
7666	db mining	Hs.313203	AW293882	6700518	UI-H-BW0-ain-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729941 /clone_end=3'	1	TTTCCCTGGTAGAGTGGCCGTTT
7667	db mining	Hs.105488	AA521017	2261560	aa70f05.s1 cDNA, 3' end /clone=IMAGE:826305 /clone_end=3'	1	AAACTAGAATTCCGGTTTCCCAAGGT
7668	db mining	Hs.125802	AA806833	2876409	oc29b10.s1 cDNA, 3' end /clone=IMAGE:1351099 /clone_end=3'	1	GGCTTCCCGCCTGTGCAGTCATTGT
7669	db mining	Hs.313274	AW295745	6702381	UI-H-BW0-aiw-g-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730834 /clone_end=3'	1	ATGTTTATATATGGAGTGT
7670	db mining	Hs.320376	BF512113	11597325	UI-H-BW1-ami-h-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070302 /clone_end=3'	1	ACAAAATATAAGGTGTACTTTGGAT
7671	db mining	Hs.315341	BE675056	10035597	7f01f10.x1 cDNA, 3' end /clone=IMAGE:3293419 /clone_end=3'	1	CCTGACTCAAACCAACCAGCTGTT
7672	db mining	Hs.320407	BF512394	11597660	UI-H-BW1-amc-f-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069456 /clone_end=3'	1	TCAAAATCCGTTACTCTTCCACAACA
7673	db mining	Hs.313347	AW297156	6703802	UI-H-BW0-ajd-b-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731329 /clone_end=3'	1	ATTGGTAGAGACGGGGTTCACCTT
7674	db mining	Hs.123298	AA809468	2878874	ob85a10.s1 cDNA, 3' end /clone=IMAGE:1338138 /clone_end=3'	1	TGTCAATTGGCTTCTTCAACTT
7675	db mining	Hs.320416	BF512570	11597749	UI-H-BW1-amf-e-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069791 /clone_end=3'	1	ACAGGGAGAGACTACACACAAGCCA
7676	db mining	Hs.309262	AI440532	4300887	CM4-NT0290-150101-684-e05 cDNA	1	GGACATGGCAGGTACTCAGTTGT
7677	db mining	Hs.313338	AW297010	6703646	UI-H-BW0-ajf-d-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731441 /clone_end=3'	1	AGCTTTGGAGAGGTTATA

Table 8

7678	db mining	Hs.315325	BE646400	9970711	7e86c01.x1 cDNA, 3' end /clone=IMAGE:3292032 /clone_end=3'	1	CCCTCCCTATCTTTTATGGGTAATT GATTATACACGGTGCTTGAATGT
7679	db mining	Hs.313172	AW293016	6699652	UI-H-BW0-aih-f-04-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729239 /clone_end=3'	1	TATGTCTTCTTACCCCAGCACCCTA ATTTAAATACAGATCCCTGAGGT
7680	db mining	Hs.313361	AW297413	6704049	UI-H-BW0-ais-b-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730208 /clone_end=3'	1	AAAACCTTGACAGTTCAATTCAACAA GCACCTATCAGGTATTCGGCAGGT
7681	db mining	Hs.313365	AW297482	6704118	UI-H-BW0-aja-a-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730920 /clone_end=3'	1	AGTGCCCATGCTGTTAGATGCTCT TCTAGCTCTGGAGATACTCAGT
7682	db mining	Hs.313358	AW297377	6704013	UI-H-BW0-air-f-11-0-Uls1 cDNA, 3' end /clone=IMAGE:2730381 /clone_end=3'	1	TGAGCTTCTGCTAGTAATTCCCTCAG GGGATTTCCATGGCGTAAGT
7683	db mining	Hs.320474	BF513180	11598359	UI-H-BW1-amj-d-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070115 /clone_end=3'	1	GAGGGTGTCTGCTAATGATTCGAA AAGTTCTCAAACACTCCGAAGT
7684	db mining	Hs.313382	AW297707	6704343	UI-H-BW0-ajh-f-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731915 /clone_end=3'	1	ACCACTGTGATGAGTTTGACAAGAG ACAAAAGGAAAGGGTGGGAGAAGT
7685	db mining	Hs.125779	AA810831	2880442	oa76d09.s1 cDNA, 3' end /clone=IMAGE:1318193 /clone_end=3'	1	GCTGGTTGTCGCTTCAAGACAGCC AACTACCAATTATTCACAGAAAGT
7686	db mining	Hs.313389	AW297882	6704507	UI-H-BW0-aju-e-07-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2733036 /clone_end=3'	1	AGTCTGTCTATTCTCTCTCTTAGCT CTGTCGTGCTCAAATTCAAGT
7687	db mining	Hs.313391	AW297905	6704541	UI-H-BW0-aju-h-11-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2733188 /clone_end=3'	1	GCCAAGGTGAGTCAAAACACTGCTCT TCAGAAAGCAATTATTTGAAAAGT
7688	db mining	Hs.309446	AI492055	4393058	tg12a01.x1 cDNA, 3' end /clone=IMAGE:2108520 /clone_end=3'	1	CATTGTCCTCCCGCTGCTCTCAG GCAATAAAATGATTGATTATTTCT
7689	db mining	Hs.313311	AW296433	6703089	UI-H-BW0-aiq-a-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730128 /clone_end=3'	1	GGTCAGAACAGGCCACAGAGACT CTGGAGGGTTCTCCTTGTGTTCT
7690	db mining	Hs.319887	BF507608	11590906	UI-H-BW1-ana-e-05-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3071720 /clone_end=3'	1	TTCAACTGCTTGGCACTGCCATGGG TACCTGAGGATAAGAGAGATGTCT
7691	db mining	Hs.255237	AW293790	6700426	UI-H-BI2-ahp-e-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2727635 /clone_end=3'	1	GGGTTGACTAAATGCACATGGGCTTA TCTTACCTCTCCAGAAATGTCT
7692	db mining	Hs.313363	AW297459	6704095	UI-H-BW0-ais-g-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730436 /clone_end=3'	1	TGCATGACCAGAAAACACTGCCGTGATA CAGTAAGCAGAGGTAGCTGCTCT
7693	db mining	Hs.320367	BF512169	11597272	UI-H-BW1-ami-c-10-0-ULs1 cDNA, 3' end /clone=IMAGE:3070074 /clone_end=3'	1	ACCTGCCAGCCAGCCCACAACATAAA ACTGTGTGACACCCAAATTATCT
7694	db mining	Hs.320440	BF512733	11597912	UI-H-BW1-amm-d-04-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070494 /clone_end=3'	1	GGTTCTGAGGTGATTCTAATATGCA GTCATGGTTAACACCTGTGATCT
7695	db mining	Hs.313374	AW297607	6704243	UI-H-BW0-ajg-e-04-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731854 /clone_end=3'	1	AAGCCTTGGACCAGCTCCGTTCTCCTGTCCC AGTTGAAAGGTTCTACCTAGCT
7696	db mining	Hs.313355	AW297325	6703981	UI-H-BW0-aih-a-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730135 /clone_end=3'	1	ACCCAAGGATGGTGTCTCTGTCCC AGTTGAAAGGTTCTACCTAGCT
7697	db mining	Hs.320420	BF512599	11597778	UI-H-BW1-amf-h-07-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069925 /clone_end=3'	1	TGGTTGAATACCGCAGGAACACCCACA GTACCCAGGGACTAATAAATAGCT
7698	db mining	Hs.118899	AA243283	1874128	zs13g11.s1 cDNA, 3' end /clone=IMAGE:685124 /clone_end=3'	1	TTAGGGCAGTGGAGAATCAGGGTGT ATCTAATAAAATTCTCTCATGGAGCT
7699	db mining	Hs.105228	AA489212	2218814	aa57d11.s1 cDNA, 3' end /clone=IMAGE:825045 /clone_end=3'	1	GCAGATGTCTCGGTATGGTTTATTATCCTCTGTTGGTCAAGGAGCT
7700	db mining	Hs.297505	BF514865	11600044	UI-H-BW1-ajj-f-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3082534 /clone_end=3'	1	TGTCTGTATTGGAGTCAGTAGTAC ACTGAAAATAATCCCGTAAAGCT
7701	db mining	Hs.320492	BF513340	11598519	UI-H-BW1-amk-b-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070050 /clone_end=3'	1	CTCCCTTCCCACCATACACACACTCC CAGCTCATTTGATTCCCTTCTCCT
7702	db mining	Hs.304837	AW292802	6699438	UI-H-BW0-ajl-f-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729615 /clone_end=3'	1	GGTGAATTGACTGGGTTCCCTCTCCC ACCTCTCTTCCGTAGCAATTCT
7703	db mining	Hs.24656	BF507762	11591060	KIAA0907 protein (KIAA0907), mRNA /cds=(26, 1720)	1	ACTAATTCCCGTGTCTGGCCCTGAAC ATGAAGATATAATGGACGATCCCT
7704	db mining	Hs.320460	BF512975	11598154	UI-H-BW1-amh-b-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069659 /clone_end=3'	1	TTAAAGGCTAAACCTACCTCAGACA CTGCTCTACCCATCCCCATCCCC
7705	db mining	Hs.313384	AW297745	6704381	UI-H-BW0-aiy-b-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730954 /clone_end=3'	1	CCCTTGTGAGAAGAAGCAGGTTCC TTTCTATGGATTGATGTGACCCCT

Table 8

7706	db mining	Hs.105105	AA419402	2079198	zu99a12.s1 cDNA, 3' end /clone=IMAGE:746110 /clone_end=3'	1	TTCTACCCATCACACAGATTCTTCCA
7707	db mining	Hs.123180	AA805419	2874169	cc13g03.s1 cDNA, 3' end /clone=IMAGE:1340788 /clone_end=3'	1	CTTAATAAAATCCATCACCTACT
7708	db mining	Hs.297396	BF515183	11600450	UI-H-BW1-anl-c-01-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3082728 /clone_end=3'	1	TCATTACTGTTGAAGGCTCTTCAA
7709	db mining	Hs.334992	AI084211	3422634	RST20881 cDNA	1	GAGAGAAAGATGAAGCTGAAACCT
7710	db mining	Hs.313273	AW295743	6702379	UI-H-BW0-alw-g-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730830 /clone_end=3'	1	GCTGTCCGTGAAAGCACTCTCAAGTC
7711	db mining	Hs.319891	BF507631	11590929	UI-H-BW1-ana-h-01-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3071856 /clone_end=3'	1	AGGAACACTGAACATAAGAACTTACT
7712	db mining	Hs.320422	BF512614	11597793	UI-H-BW1-amg-a-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069822 /clone_end=3'	1	CTCCGTAAATCCAGCACTGGAGCTT
7713	db mining	Hs.319872	BF507414	11590721	UI-H-BW1-amz-a-11-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3071517 /clone_end=3'	1	CTAGGGTGCGGAGAATGGTGTGAT
7714	db mining	Hs.264120	AI523641	4437776	601436078F1 cDNA, 5' end /clone=IMAGE:3921187 /clone_end=5'	1	TTGGTACACAGCTGAAATAGACGGAT
7715	db mining	Hs.105284	AA491263	2220436	aa49d04.s1 cDNA, 3' end /clone=IMAGE:824263 /clone_end=3'	1	GCAACAATTCTTGGAAAGTGACTCT
7716	db mining	Hs.124376	AA831043	2904142	cc58h02.s1 cDNA, 3' end /clone=IMAGE:1353939 /clone_end=3'	1	CTAGGGTGCCTGACGGGCTTTCAA
7717	db mining	Hs.309144	AI384035	4196816	td05c02.x1 cDNA, 3' end /clone=IMAGE:2074754 /clone_end=3'	1	AAGCGACTCATTATGAAGAAGAAT
7718	db mining	Hs.301325	BF514004	11599183	UI-H-BW1-emv-e-04-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3071311 /clone_end=3'	1	GCACTCCAGCCTGGGCAACAAGAGC
7719	db mining	Hs.319904	BF507742	11591040	UI-H-BW1-anc-f-02-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3072122 /clone_end=3'	1	GAAACTCTGCCCTCCAATAAAAT
7720	db mining	Hs.320092	AI392740	4222287	tg23f02.x1 cDNA, 3' end /clone=IMAGE:2109627 /clone_end=3'	1	GCAGCTTACGCTTACAGGAGGCTTG
7721	db mining	Hs.313371	AW297578	6704214	UI-H-BW0-ajg-b-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731708 /clone_end=3'	1	ACCAACCCATATGGACAACTTGATCTT
7722	db mining	Hs.320444	BF512784	11597963	UI-H-BW1-amm-h-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070698 /clone_end=3'	1	GAACCTCTAGCTTACAGACCTGTG
7723	db mining	Hs.320473	BF513155	11598334	UI-H-BW1-amj-b-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070013 /clone_end=3'	1	AATGTAGCTGACATTGGAGCCACCGC
7724	db mining	Hs.320419	BF512597	11597776	UI-H-BW1-amf-h-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069921 /clone_end=3'	1	CCATAGAAGAAGGCTAAACTGTG
7725	db mining	Hs.320365	BF512157	11597260	UI-H-BW1-aml-b-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070026 /clone_end=3'	1	CTTCACTGACGATCTGAGACACTAGG
7726	db mining	Hs.299471	BF513893	11599072	UI-H-BW1-amq-d-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070874 /clone_end=3'	1	CAGCTTGGAAAGGGTGGAGTGGT
7727	db mining	Hs.313368	AW297544	6704180	UI-H-BW0-aja-g-01-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731200 /clone_end=3'	1	GCCCCTGGTGGTTGGAAAAGTGTCT
7728	db mining	Hs.105170	AA481410	2210962	zv02g12.s1 cDNA, 3' end /clone=IMAGE:746374 /clone_end=3'	1	GAATCCAATAAAAGGAAAGCGGTG
7729	db mining	Hs.313251	AW295130	6701766	UI-H-BW0-alf-h-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730495 /clone_end=3'	1	CAACAGTGGCAAGAGTAGCCAGCCC
7730	db mining	Hs.297392	BF514201	11599380	UI-H-BW1-ani-d-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3082401 /clone_end=3'	1	ATAGGACGGAATGAAAATCAAGGTG
7731	db mining	Hs.122417	AA761212	2810142	nz20c03.s1 cDNA, 3' end /clone=IMAGE:1288324 /clone_end=3'	1	CATCCTTAGATGCCAGTCTTCACTT
7732	db mining	Hs.297469	BF512785	11597954	UI-H-BW1-amm-h-11-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070700 /clone_end=3'	1	GGGTATTTCCCTGCCCTCAGTGTG
7733	db mining	Hs.313275	AW295750	6702386	UI-H-BW0-alw-h-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730868 /clone_end=3'	1	TCTAAATGTTGCCCTCAGAGATGCA

Table 8

7734	db mining	Hs.313173	AW293031	6699567	UI-H-BW0-aih-g-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729299 /clone_end=3'	1	AGTTCTTGTAAACAGTTAAACTTCCTT GCCAGCTCTCAGGTTACACTGG
7735	db mining	Hs.320386	BF512295	11597474	UI-H-BW1-amb-e-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069388 /clone_end=3'	1	GTGTGTAAATGAGTGTCAGATCTTT CTTGAAAACAGGTTGGATTGGGG
7736	db mining	Hs.320429	BF512664	11597843	UI-H-BW1-amb-f-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069844 /clone_end=3'	1	AGGGTCCACAAGGAAATTTCTT AAAGTAACTCCCTGATTCGCGGGG
7737	db mining	Hs.123352	AA811133	2880744	oa98b10.s1 cDNA, 3' end /clone=IMAGE:1320283 /clone_end=3'	1	GCTCCCTATGCCGTGTAGCAGAAT CTAAAAGATAATCATGTGAACGGG
7738	db mining	Hs.320389	BF512323	11597502	UI-H-BW1-amb-g-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069497 /clone_end=3'	1	TTGCTTGTCTTCTTTATCTCCCTAT GTTTCATCTTAGTGCAGGCAGGG
7739	db mining	Hs.120563	AA741116	2779708	n204f08.s1 cDNA, 3' end /clone=IMAGE:12856823 /clone_end=3'	1	ACAGTTGCCTTGAGATTCTGTATTT CTGCATGAAATAATCCATAAGGG
7740	db mining	Hs.320373	BF512098	11597310	UI-H-BW1-ami-f-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070222 /clone_end=3'	1	GTCCTTGGAAAGGTAACACTTGTGATT GGAACCACTCTCAAGCTGAACGG
7741	db mining	Hs.320490	BF513327	11598506	UI-H-BW1-amk-a-07-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069996 /clone_end=3'	1	ATTCATTCAATTCAACAAGCACTT AAAAACAAATGCCGTGTGCCAGG
7742	db mining	Hs.313290	AW296074	6702710	UI-H-BW0-aiu-h-07-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730852 /clone_end=3'	1	CACACCCAGCCCCATTCAAAGGAC TATAAAATCTACACCCCAGTCACG
7743	db mining	Hs.320390	BF512330	11597509	UI-H-BW1-amb-h-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069537 /clone_end=3'	1	GGCATAGTAGTGCTAACAGAGGTG GAAGTAGTGAAGGGAGTTTGAACG
7744	db mining	Hs.297397	BF507606	11590904	UI-H-BW1-ana-e-02-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3071714 /clone_end=3'	1	CTAGTCTGCCACCCACCTCCCCAAGT ATTACCCCTCTAACAGTCCTGCTAG
7745	db mining	Hs.309256	AI373161	4153027	qz13a01.x1 cDNA, 3' end /clone=IMAGE:2021352 /clone_end=3'	1	AGATAAGCAGGATAAAACAGACAGGT TGGATTGTGATCAGCTATGGAG
7746	db mining	Hs.343303	BF513322	11598501	UI-H-BW1-amk-a-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069986 /clone_end=3'	1	GATGGCTAGGACAAGATGATTACAA GAGCGTGGCGGGAGGGACGGCGAG
7747	db mining	Hs.301870	BF507614	11590912	UI-H-BW1-ana-f-03-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3071764 /clone_end=3'	1	CCGTGTCTGGATTGTGTCTTAATT CTAAGGTGCACATACTCTATAAG
7748	db mining	Hs.300479	AW452510	6993286	UI-H-BW1-ame-a-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069598 /clone_end=3'	1	GTATCTCTGCACCTCACTACTACCCT TCACCTCTGGAGACCTGGGCAAG
7749	db mining	Hs.320387	BF512301	11597480	UI-H-BW1-amb-e-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069401 /clone_end=3'	1	AACACACCACCAAAACATTCTCCCAT CCTTCTCACCAACCAGCTACAAAG
7750	db mining	Hs.122854	AA292626	1940611	zs57h08.r1 cDNA, 5' end /clone=IMAGE:701631 /clone_end=5'	1	ACAATTGGAGTTGGGCTGTACACAC CTGAAGTGTCAACCAACAGAAAG
7751	db mining	Hs.300488	AW453029	6993805	UI-H-BW1-ama-c-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069306 /clone_end=3'	1	TTAGGGCAAAAGTCCTAGTGGCGGC AGCTTCTGTCTAGACCCCTGGTTC
7752	db mining	Hs.335081	AI380942	4190807	tg18c08.x1 cDNA, 3' end /clone=IMAGE:2109134 /clone_end=3'	1	AGTGATGCTTGCCTTTCGCTTCCCT AAAGATGTCAATTGAAACAAAGTC
7753	db mining	Hs.313822	AW452916	6993692	UI-H-BW1-amd-b-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069267 /clone_end=3'	1	CCCAGCTTCATTAATGTGAATGGTG CAGACACCTCTAGCTATAGACTC
7754	db mining	Hs.309486	AI523959	4438094	tg98t09.x1 cDNA, 3' end /clone=IMAGE:2116841 /clone_end=3'	1	GAGCCAAAGATTGGGCCACTGCACTC CAGCCTGGGTGACAGAGTGAGACTC
7755	db mining	Hs.303926	AI084223	3422646	oy72g05.x1 cDNA, 3' end /clone=IMAGE:1671416 /clone_end=3'	1	GAGCCGAGATTGCATCACTGCACTCC AGCCTGGTCAACAGAGCGAGACTC
7756	db mining	Hs.313170	AW292942	6699578	UI-H-BW0-alg-f-11-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729252 /clone_end=3'	1	TTCAGTCATGCAGCAACATCCGCTTA ATGCCTCTAACAGTCAGAACACTC
7757	db mining	Hs.313795	AW452553	6993329	UI-H-BW1-ame-e-11-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069788 /clone_end=3'	1	GGTCCTCTCTCTACTCTCCCTAG TAATCAACCACCAAGCCTAAATC
7758	db mining	Hs.319883	BF507567	11590865	UI-H-BW1-amr-h-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3071078 /clone_end=3'	1	TTGTTTGTGTTATTTATTTATTTAGG CGAGCGTGTCTGCTGTGTTG
7759	db mining	Hs.320476	BF513187	11598366	UI-H-BW1-amj-e-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070155 /clone_end=3'	1	TGCCCATTTACATCTAACAGAGG TAGAGCTCCCTGGTGTTCCTGC
7760	db mining	Hs.313828	AW453000	6993776	UI-H-BW1-ama-a-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069200 /clone_end=3'	1	TGCTCTGCTCTCCCAAATCAAGGAA TGAGATCTTGTAAACAGAACACTC

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7761	db mining	Hs.120251	AA731386	2753542	nz86f07.s1 cDNA, 3' end /clone=IMAGE:1302373 /clone_end=3'	1	TGGCACCAACTTACACTTCCAGAAGA GAGTGGTCAGGAAATTACTATGC
7762	db mining	Hs.313392	AW297908	6704544	UI-H-BW0-ajn-a-04-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732071 /clone_end=3'	1	AACTTTGGGAAGTGAGACTCTGTCTT GGGTTTTGATAATAATGTGGC
7763	db mining	Hs.343320	BF512697	11597876	UI-H-BW1-amm-a-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070346 /clone_end=3'	1	CCGAGAAAAGTACGGCTGGAGCGGAC TGAGGAGACGAAATTGAGTCGC
7764	db mining	Hs.304176	AI540182	4457555	td10f04.x1 cDNA, 3' end /clone=IMAGE:2075263 /clone_end=3'	1	CGAAGAAAAGATTGGATGCAGAATTG TTGCCTAACCTGGTGACAAGAGC
7765	db mining	Hs.320425	BF512629	11597808	UI-H-BW1-amg-c-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069700 /clone_end=3'	1	AGTGCTGTGATCCACCCCCCTTACC TCCCCTCAAGTGACAATGTAAGC
7766	db mining	Hs.313236	AW294711	6701347	UI-H-BW0-aim-b-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729808 /clone_end=3'	1	AGAAAGTTAGGAGTCGGCAACCTAA GGAGGAGTTCTCATCTCTCC
7767	db mining	Hs.313379	AW297666	6704302	UI-H-BW0-ajh-c-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731755 /clone_end=3'	1	TGTCACAAAGATGAAGCAAGTGGCT CAGGGAAACGTGCTCAGAAACCTCC
7768	db mining	Hs.123341	AA810927	2880538	oa77d07.s1 cDNA, 3' end /clone=IMAGE:1318285 /clone_end=3'	1	GCAAAGTAAAGTTTCCCTTGGCC CTAAAATATGAAAGCAAAGCATCC
7769	db mining	Hs.313208	AW293991	6700627	UI-H-BW0-alk-h-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729726 /clone_end=3'	1	CCCTGTCCATCTTCTGTCTTCTATC CAGCCCTCCCTCTCCCTTTGCC
7770	db mining	Hs.123344	AA811024	2880635	oa82g05.s1 cDNA, 3' end /clone=IMAGE:1318808 /clone_end=3'	1	CCACGGAGGGCTCCCCATCTAAAGG GAGTTAATAACAAAGGAATGGCC
7771	db mining	Hs.320450	BF512839	11598018	UI-H-BW1-amu-e-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3071322 /clone_end=3'	1	CAATTGGTACATTCTCGGAAACCT TGCCCAATTTCTCAGGAAGCC
7772	db mining	Hs.313369	AW297549	6704185	UI-H-BW0-ajg-g-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731214 /clone_end=3'	1	AGGGTGTCCCTGTGATTTAAATTC ACTATCTAGCTGCCCCATCCCCC
7773	db mining	Hs.297527	BF515924	11601103	UI-H-BW1-aoa-e-01-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3084001 /clone_end=3'	1	CTTATATTATGTTTCTCTGTGACAAG CACCTCACCTCCAAACCCACCC
7774	db mining	Hs.287513	BF515498	11600677	UI-H-BW1-ann-g-04-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3082950 /clone_end=3'	1	GAGAATTCAAATTAAATGCAGAGTC TAGGCCACCCCTGGCATACCAACCC
7775	db mining	Hs.105218	AA488881	2218483	aa55f06.s1 cDNA, 3' end /clone=IMAGE:824867 /clone_end=3'	1	ACAACCAATGCCCTCACACTTAAGCTC CTAGAACGTCACTAGGGACAGACC
7776	db mining	Hs.309447	AI492062	4393065	tg12a11.x1 cDNA, 3' end /clone=IMAGE:2108540 /clone_end=3'	1	GCCCTCACCAAGTCAATCATGCTG GCACCTTATCTGGACTTTCAACC
7777	db mining	Hs.309483	AI523758	4437893	tg94e10.x1 cDNA, 3' end /clone=IMAGE:2116458 /clone_end=3'	1	AGGGTAAGAGTCCAGACCTGACTG GACAATAAGTGAAGACTGTCTCTAC
7778	db mining	Hs.343333	BF515310	11600412	UI-H-BW1-ank-g-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3082577 /clone_end=3'	1	CTCCGTCTGCCGCCCTCGTAGCCAC AGCGACTTTGAAAGTGATTTGAC
7779	db mining	Hs.309687	AI401187	4244274	tg26h10.x1 cDNA, 3' end /clone=IMAGE:2109955 /clone_end=3'	1	CCCTGGAGAAGGAGGGTGATTTATT TCAACTTCTGATTACCACCGAC
7780	db mining	Hs.314730	AI523958	4438093	tg98f08.x1 cDNA, 3' end /clone=IMAGE:2116839 /clone_end=3'	1	GATTGTTGAGCCTGGGAGTCCACA CCAGCCTGGGCTACATAGGGAGAC
7781	db mining	Hs.313337	AW297006	6703642	UI-H-BW0-ajf-c-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731409 /clone_end=3'	1	CTGCTCTAGACTGAGCACAGCCACTG ACAGGTGACCTTCAGAACCTC
7782	db mining	Hs.116455	AA649141	2575570	ns32g12.s1 cDNA, 3' end /clone=IMAGE:1185382 /clone_end=3'	1	ACCCCTGCTTACTGTGACAGACATA TAGTTGTACATACATAAAACCCAC
7783	db mining	Hs.123313	AA810089	2879495	od12f12.s1 cDNA, 3' end /clone=IMAGE:1367759 /clone_end=3'	1	ACCTAACAGAAATTGGATTGGGTT GTCTAAATACACCCCTGGTGGGTTA
7784	db mining	Hs.319868	BF507353	11590660	UI-H-BW1-amx-c-04-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3071239 /clone_end=3'	1	GCCTTCCCACCAACAGTTATGTGA TTCCCTGCCCTACCTTCTCTGGATA
7785	db mining	Hs.123342	AA811005	2880616	oa73g11.s1 cDNA, 3' end /clone=IMAGE:1317956 /clone_end=3'	1	TCCCATTCGATGCTCGTATATTGAA AGCTGCCCTACTTCTCTGGTA
7786	db mining	Hs.313288	AW296061	6702697	UI-H-BW0-aiu-g-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730802 /clone_end=3'	1	GGCAGGGGATGAACCAGATAATTCC AGCCCTTCTGGTAGCTCTCGTA
7787	db mining	Hs.308998	AJ356553	4108174	qz27h12.x1 cDNA, 3' end /clone=IMAGE:2028167 /clone_end=3'	1	GCTTAGGAGTTGGGACCAGCCTGG GTAACATAGTGAACACCTGTCTCTA

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7788	db mining	Hs.313328	AW296796	6703432	UI-H-BW1-ajb-e-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731115 /clone_end=3'	1	TTGCAGCTATTTCAAGTTGTAAGAAA TGAACCTTCAACACATAGGGCTA
7789	db mining	Hs.320462	BF512985	11598165	UI-H-BW1-amh-c-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069707 /clone_end=3'	1	TCTCTTGCCACAGGGATTCCCTCAA GCTGGAATCACCATTCCCTCTA
7790	db mining	Hs.297514	BF516300	11601479	UI-H-BW1-anz-e-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3084010 /clone_end=3'	1	CCCACCCACCAGTAGGTTGTATTCA ACTGAACCATTCAGGAGCACCTA
7791	db mining	Hs.124358	AA830650	2903749	oc52g02.s1 cDNA, 3' end /clone=IMAGE:1353362 /clone_end=3'	1	GAACCCAGCTAACGCCACACCCAGATT CTGACCCAGGGATACTCTGAATA
7792	db mining	Hs.313345	AW297163	6703769	UI-H-BW0-ajd-a-04-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2731278 /clone_end=3'	1	GTGTGTGCTGGCGTGCCTTATAGGT GTGCGTGTTCCTGTCAGTTTGA
7793	db mining	Hs.320484	BF513246	11598425	UI-H-BW1-amo-b-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070426 /clone_end=3'	1	AGGAAAACTCAGAAATAATTCTGCC CCCTGGATTCTTAAGATTGTGA
7794	db mining	Hs.105130	AA482030	2209708	zu98g04.s1 cDNA, 3' end /clone=IMAGE:746070 /clone_end=3'	1	GTGGAAGAAATCCTACAACGAAACACT ATAAAGTCTGCACCTAGATCTGA
7795	db mining	Hs.104176	AA214530	1813155	zr92a06.s1 cDNA, 3' end /clone=IMAGE:683122 /clone_end=3'	1	GGCCTAGGTTCCAGCATTCACTCATC AAGCTTGTACAGAAATAATGA
7796	db mining	Hs.121118	AA721101	2737236	nz67a01.s1 cDNA, 3' end /clone=IMAGE:1300488 /clone_end=3'	1	CCCCATTGGAGTCTAGTCAAACAG CAGCTCTTGAGTTACCATGGGA
7797	db mining	Hs.313313	AW296455	6703091	UI-H-BW0-aiq-c-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2730224 /clone_end=3'	1	AAGGCTTGTAACTGTAGGCCCCGTGA CTACACTGTGCTATACTGGTAGA
7798	db mining	Hs.335116	AI524072	4438207	th01d07.x1 cDNA, 3' end /clone=IMAGE:2117005 /clone_end=3'	1	CACTTTGGGAGGCAGAGGTGAGCAG ATCACTTGAGGCCAGGAGTTGAGA
7799	db mining	Hs.309130	AI382229	4195010	td04d04.x1 cDNA, 3' end /clone=IMAGE:2074663 /clone_end=3'	1	GGATCACTTGAAGCCAGCAGTTGAG ACCAGCCTGGCAATAAAATGAGA
7800	db mining	Hs.297504	BF514819	11599998	UI-H-BW1-anj-b-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3082338 /clone_end=3'	1	TCAGTTGTGATGGGATTCTTGATGG ATGAGATGTGCTGTGACAGAGA
7801	db mining	Hs.297473	BF513074	11598253	UI-H-BW1-amn-c-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070445 /clone_end=3'	1	CCTCTAGAACTGGAACCAAGACTGC TCACATCAGAGTAAAGGTGAAGA
7802	db mining	Hs.313168	AW292924	6699560	UI-H-BW0-ajg-d-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729144 /clone_end=3'	1	GCTCACCCCTGCACCTCCCTCCAAA TCTGCTGTCACATTTCTCAAAGA
7803	db mining	Hs.319885	BF507583	11590881	UI-H-BW1-ana-b-03-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3071572 /clone_end=3'	1	TTCCCTGTCTCCATGTTGGTCAAGA TTGCCATTGCTTCTGAGTTCA
7804	db mining	Hs.320411	BF512514	11597693	UI-H-BW1-amc-h-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069570 /clone_end=3'	1	CTGGTCTAGTGCAGTCCTCACTT TCCTGGTGTGGTTATCTTCA
7805	db mining	Hs.116501	AA651832	2583484	ns40b05.s1 cDNA, 3' end /clone=IMAGE:1186065 /clone_end=3'	1	TGACATGATTACCTGACTGATGTT TCCTCCATTAGACTGAATGCTTCA
7806	db mining	Hs.320438	BF512719	11597898	UI-H-BW1-amm-c-01-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070440 /clone_end=3'	1	TGGCAAAAGCCTAACACTGACTCAT CCCATTCTATCAGCACAAACTTCA
7807	db mining	Hs.319888	BF507612	11590910	UI-H-BW1-ana-e-12-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3071734 /clone_end=3'	1	GTTTACAAGGGATACTAGTCTCTGGA GGGACGAAGGAGGCTGTGTTGCA
7808	db mining	Hs.250726	AW298545	6705181	UI-H-BW0-ajm-g-01-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732352 /clone_end=3'	1	TCCTCAACTCGGAGATTCTGTATGG AGAGAACTCAATTCTATATTGCA
7809	db mining	Hs.120738	AA749236	2789184	nx89c09.s1 cDNA, 3' end /clone=IMAGE:1270384 /clone_end=3'	1	ACATTTCTTAGGTGTGAGTGGTGAAG GAAAAATAGTGGAAAGATGTCTGCA
7810	db mining	Hs.320404	BF512350	11597616	UI-H-BW1-amc-b-01-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069264 /clone_end=3'	1	TCAGGAGGCTTGGAAAGACTCAAGGT TTCTACACTATGGGAAATAAGGCA
7811	db mining	Hs.319880	BF507510	11590808	UI-H-BW1-amr-c-04-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070831 /clone_end=3'	1	GTTTCACTTGTGATACTAACTATTGT TTTTCTCCCCATGCCAGAGCA
7812	db mining	Hs.320371	BF512091	11597303	UI-H-BW1-aml-f-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070208 /clone_end=3'	1	AGCCAAGGGAGCATATTCTCTTA TTTAACCTCTCCGTAGGCAGCA
7813	db mining	Hs.307837	AI052783	3308774	oy78h09.x1 cDNA, 3' end /clone=IMAGE:1672001 /clone_end=3'	1	AGAAGGACCCCTGGTTGAGAACAC GGTTGTATAGAAAGGAATTGAAGCA
7814	db mining	Hs.124383	AA831706	2904805	oc85b04.s1 cDNA, 3' end /clone=IMAGE:1356463 /clone_end=3'	1	TTGACTGCCATAGCCAAGAGTTAATA TAGTTGCGTTCTTAAGGAAGCA
7815	db mining	Hs.123304	AA809672	2879078	nz99b08.s1 cDNA, 3' end /clone=IMAGE:1303575 /clone_end=3'	1	CTTACTGTGCTTAACTGTTGCTTCTGCTATGCTATGTTCCA

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7816	db mining	Hs.123368	AA811539	2881150	ob45d08.s1 cDNA, 3' end /clone=IMAGE:1334319 /clone_end=3'	1	TGCAGTTAGGAGTGTGGACACTCTGC CCATCTCCATTGAATTAATTCGA
7817	db mining	Hs.313176	AW293164	6699800	UI-H-BW0-aii-c-01-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729448 /clone_end=3'	1	ACTGGGTTCTATCCCCACGATAACT TGTATGTATATGCCAATATCCCA
7818	db mining	Hs.313171	AW292976	6699612	UI-H-BW0-aii-b-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729055 /clone_end=3'	1	AGCTAGAAAATGTCCTTTCTCTT TGAGGTCTTACCAAGGCCA
7819	db mining	Hs.343308	BF508886	11592184	UI-H-BI4-aos-a-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3085732 /clone_end=3'	1	ATCACCAATCTTATTTAGCACTGTGG ATGCCGTTTGCAAATGTCAACCCA
7820	db mining	Hs.320468	BF513104	11598283	UI-H-BW1-amn-e-10-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070555 /clone_end=3'	1	TGACTTAAGGTTGGAATATCTCTAC TACTCCCCTGCTCCTGGACCA
7821	db mining	Hs.120585	AA743221	2782727	ny21c06.s1 cDNA, 3' end /clone=IMAGE:1272394 /clone_end=3'	1	TGTGTTTGCATGGTTACTGATGA GACAGCAAAATGAGACAGGACCA
7822	db mining	Hs.297468	BF513126	11598305	UI-H-BW1-amn-g-09-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070649 /clone_end=3'	1	TGGCGAGCCAGTCTCTGGATGGGAT TCTGATCACAGAACAGTTCTCATACA
7823	db mining	Hs.313205	AW293932	6700568	UI-H-BW0-aii-b-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2729426 /clone_end=3'	1	TGCCCCATCCTTGCTGTTTCTCTTT CAGTCATGGCCTATTGGAGACAA
7824	db mining	Hs.343329	BF515646	11600825	UI-H-BW1-anu-d-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3083555 /clone_end=3'	1	CTCAACCTTGGCCCTAAACTAACAGT GACAGGGAGTCCCCAGCCTCACAA
7825	db mining	Hs.319906	BF507755	11591053	UI-H-BW1-anc-g-07-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3072180 /clone_end=3'	1	TCCTGACCGTTGACAGAGAGCTTTA CAGAAGTCTTAGGCAGTACACACA
7826	db mining	Hs.320465	BF513053	11598232	UI-H-BW1-amn-a-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070355 /clone_end=3'	1	AGTGTGTGGCACCCAGGGATCACTG TATGAGAATTCTGAACAAACAACAA
7827	db mining	Hs.320430	BF512667	11597846	UI-H-BW1-amg-f-06-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069850 /clone_end=3'	1	GCTGAAAGTCCCTCCTACTCATCT TCCCTCTCAATACAACAACAA
7828	db mining	Hs.120718	AA748539	2788497	ny05h12.s1 cDNA, 3' end /clone=IMAGE:1270919 /clone_end=3'	1	GCCAGTTGGCACCATTTATGAAACAC ACCACCTTGTAAACCAGTGAATTAA
7829	db mining	Hs.320472	BF513154	11598333	UI-H-BW1-amj-b-02-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070011 /clone_end=3'	1	TCAACCTAGCACAGTGCCTGGCTGAT AGGTGTTGAATATTCACACTCAA
7830	db mining	Hs.319899	BF507695	11590993	UI-H-BW1-anb-h-05-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3071865 /clone_end=3'	1	GCAACCCCTGCCCCCTGCAAAGAGAT ATTGTGACAAAGATATTCACTGAA
7831	db mining	Hs.124932	AA825273	2898575	oc67a02.s1 cDNA, 3' end /clone=IMAGE:1354730 /clone_end=3'	1	TAACATTCTGGCACAGTCCCTGGCA TAGGGTAGATAATAATGGTGGAA
7832	db mining	Hs.313354	AW297308	6703944	UI-H-BW0-aji-h-03-0-Ui.s1 cDNA, 3' end /clone=IMAGE:2732020 /clone_end=3'	1	TCTCTAACCATCAAGGAAGGTCAGG GCCATGTATCTTTAGGGAGAA
7833	db mining	Hs.127178	AA938725	3096753	oc10g07.s1 cDNA, 3' end /clone=IMAGE:1340508 /clone_end=3'	1	TTCCACAAACTCAGGTGTGCAAGAAA CAATGCATTACTTTATTTCAAGAA
7834	db mining	Hs.320445	BF512786	11597985	UI-H-BW1-amn-h-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070702 /clone_end=3'	1	CAGGAGTTGAGACCAGCCTGGCA ACATAGTAAGTCTCCATCTTCAA
7835	db mining	Hs.319902	BF507708	11591006	UI-H-BW1-anc-b-02-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3071930 /clone_end=3'	1	TCCCTAGTCCTGGAGACTCGGGAACT AAAACAATCAATTCCCTGAGCAA
7836	db mining	Hs.104348	AA251338	1886301	zs08a06.s1 cDNA, 3' end /clone=IMAGE:684562 /clone_end=3'	1	TCCTCTTCACTGGAGACCCCTCCCTG TCACAGCACAATGTGGGTAATAAA
7837	db mining	Hs.320442	BF512761	11597940	UI-H-BW1-amm-f-08-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3070598 /clone_end=3'	1	CAGAACAGGCCACAGTGTGAAAG GTGCTGCTGAACAAAGATAATAAA
7838	db mining	Hs.320470	BF513152	11598331	UI-H-BW1-amj-a-12-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3069983 /clone_end=3'	1	GAGTCAGCAACACTGGCTCTTGGC TTGGTTGATGCTTTGAAGTGA
7839	db mining	Hs.300359	BF516423	11601602	UI-H-BW1-aoe-h-05-0-Ui.s1 cDNA, 3' end /clone=IMAGE:3084512 /clone_end=3'	1	TAAGGATGTATCCCTATGGGCAGGAA ACCCAATTCTAAGAAAATTACAAA
7840	db mining	Hs.309152	AI392970	4222517	tg22d05.x1 cDNA, 3' end /clone=IMAGE:2109513 /clone_end=3'	1	GCCACTGCACCTCCAGCCTGGCAAC AGAGCGAGACCTGACTCTTAAAA
7841	db mining	Hs.122448	AA761767	2810697	nz31e08.s1 cDNA, 3' end /clone=IMAGE:1289414 /clone_end=3'	1	CACAAACCCCCAAAAGGCTGCATTGCA TAACATGTATTTGTTGAATGAAA
7842	db mining	Hs.319874	BF507452	11590750	UI-H-BW1-amz-e-06-0-Ui.s2 cDNA, 3' end /clone=IMAGE:3071699 /clone_end=3'	1	GGGGTCCTTGCTCACAGAGCTCCCA AGATGGTGGTGGGGCACTTCCAAA
7843	db mining	Hs.104177	AA214542	1813167	zr92b09.s1 cDNA, 3' end /clone=IMAGE:683129 /clone_end=3'	1	TCCCTCTATAGGTTAAAGACCTGTT GTCTGAAATGTGTTGAAACCTGTCT

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7844	db mining	Hs.104182	AA521405	2261948	aa68c06.s1 cDNA, 3' end /clone=IMAGE:826090 /clone_end=3'	1	GCTGCCGTGTCCTTGGCATTTCAG CATGACTATGTTTTGTAATGT
7845	db mining	Hs.255522	AW296182	6702818	UI-H-BI2-ala-c-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2728680 /clone_end=3'	1	CCGAAGGCCCGTGTGGCGCTTCCTC TATTCTGTAGAGTGGTAGTTGTT
7846	db mining	Hs.124928	AA765668	2816908	oa04f02.s1 cDNA, 3' end /clone=IMAGE:1303995 /clone_end=3'	1	AAAGAGGTAAACGCAAGTCTCTCTT GTAGGTGGGGCTACAGGTGACTTT
7847	db mining	Hs.320388	BF512314	11597493	UI-H-BW1-amb-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069453 /clone_end=3'	1	TGGTCTCACGCCCTGGGTGAAACAGAG AAGGGGTCTAATTGGTCTTTGTT
7848	db mining	Hs.123161	AA807319	2876895	oc38bd1.s1 cDNA, 3' end /clone=IMAGE:1351945 /clone_end=3'	1	TGTTCTGGCACCCCTGCACTGTCAGG CTATATCATTCGTTGTTCTT
7849	db mining	Hs.120608	AA743877	2783228	ny25b04.s1 cDNA, 3' end /clone=IMAGE:1272751 /clone_end=3'	1	TCTCATTTCCTTCCTAGCTGTGATG CAAAGTGTCAAGTGGTCCCCATCTT
7850	db mining	Hs.120654	AA741010	2779602	ny99a10.s1 cDNA, 3' end /clone=IMAGE:1286394 /clone_end=3'	1	TGTCCAACCTCCTTGTACAAC AAAGAACATGCCTAGGGATTCAACTT
7851	db mining	Hs.330148	BE676227	10036768	xm80f05.x1 cDNA, 3' end /clone=IMAGE:2690529 /clone_end=3'	1	CAAGTGGCCTGGTGTAAATCTTG CCCTAAATTGTAACTCACATGATT
7852	db mining	Hs.120259	AA731522	2753878	nw59h09.s1 cDNA, 3' end /clone=IMAGE:1250945 /clone_end=3'	1	ACCAACCAGTGGTGTGCTGGAGCTG TCTCATACTATCTTGAGAGTCCATT
7853	db mining	Hs.124333	AA829233	2902332	od05a10.s1 cDNA, 3' end /clone=IMAGE:1358298 /clone_end=3'	1	AGCACTTGCTTGTCCAGACATTGT CCTTAGCTCCTTGTGTAAATT
7854	db mining	Hs.124281	AA825840	2899152	od59d02.s1 cDNA, 3' end /clone=IMAGE:1372227 /clone_end=3'	1	TGCAGCAAAAATTGAATTTCATAGGC CATTCAAGTGTCTCTGCGATAATT
7855	db mining	Hs.120716	AA748500	2788458	ny01h10.s1 cDNA, 3' end /clone=IMAGE:1270531 /clone_end=3'	1	CCAGGAATGGAATAACGCCAACCCA GGTTAGGCACCTCTATTGAGAATT
7856	db mining	Hs.320428	BF512663	11597842	UI-H-BW1-amg-f-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069842 /clone_end=3'	1	AGGAAATTGGTTGAAGTCGTTTCT CTTGTTAGTCTCATGTTAAGCTGT
7857	db mining	Hs.123593	AA814828	2884424	ob73d07.s1 cDNA, 3' end /clone=IMAGE:1337005 /clone_end=3'	1	TCGCCTGGGAGAATTAAATCTAA GTCGCTGGAAAGTCCTTGTATGT
7858	db mining	Hs.120214	AA730985	2752189	nw67a04.s1 cDNA, 3' end /clone=IMAGE:1251630 /clone_end=3'	1	ACCTGTAGGAAGGGTTGTGAATATT CTGTTGCTCTGAATTATTAGCGGT
7859	db mining	Hs.123365	AA811469	2881080	ob83c11.s1 cDNA, 3' end /clone=IMAGE:1337972 /clone_end=3'	1	TGAGAGGATCTTGAGACATTCTGTG TTATTGCCCCTATGTTTAGGT
7860	db mining	Hs.127156	AA838155	3096268	oc10a09.s1 cDNA, 3' end /clone=IMAGE:1340440 /clone_end=3'	1	TCCAAGCATGAGACAAGTACCCACCA GTGGTTCAAGGAGATGATTTAGGT
7861	db mining	Hs.320486	BF513276	11598455	UI-H-BW1-amo-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070560 /clone_end=3'	1	ACAAGACAGCAGCCTTCCCAGAAATGT CACTACTAAGAATTATCAGAGGT
7862	db mining	Hs.343330	BF514718	11599897	UI-H-BW1-ans-a-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3083063 /clone_end=3'	1	GCTGCCAAACTCCATTTATTACCCCTCACTAACATCACTCCCTCCT
7863	db mining	Hs.123584	AA814349	2883945	nz06h06.s1 cDNA, 3' end /clone=IMAGE:1287035 /clone_end=3'	1	ACATTGCAATGCACTTGATGTAAG GTTGTGAGGATGTTGACTCTCCT
7864	db mining	Hs.123376	AA811751	2881362	ob80e12.s1 cDNA, 3' end /clone=IMAGE:1337710 /clone_end=3'	1	TCCCCCTTCTAACACCAATTGGGA ACATCACTACTTGTATATTACCT
7865	db mining	Hs.122860	AA766374	2817612	oa36b03.s1 cDNA, 3' end /clone=IMAGE:1307021 /clone_end=3'	1	TCAAGACCCCTTAAAGTAAGTAACTC CCAAGGAAATGTTAGTTAGTCCT
7866	db mining	Hs.105268	AA490812	2219985	aa49e05.s1 cDNA, 3' end /clone=IMAGE:824288 /clone_end=3'	1	AACCCACAATCCAACCTCCCTGATGA GGATGATCATAACAAACAACTCACT
7867	db mining	Hs.297465	BF512677	11597856	UI-H-BW1-amg-g-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069894 /clone_end=3'	1	TTTGAAGCCTCTGGTACTTCCCTTC CCAAACCCAGTCACAGGAAACACT
7868	db mining	Hs.127167	AA938326	3096437	oc11c08.s1 cDNA, 3' end /clone=IMAGE:1340558 /clone_end=3'	1	TTGGAGGTTAACAGTATTCTTGAG TGGTGTGATTAAGGTGCTTTAT
7869	db mining	Hs.123361	AA811359	2880970	ob82a07.s1 cDNA, 3' end /clone=IMAGE:1337844 /clone_end=3'	1	CCAAACCTCCAGAACTGCCTATCTAAC TCATCTGTTGATGGAATGCTAT
7870	db mining	Hs.105282	AA491247	2220420	aa49b01.s1 cDNA, 3' end /clone=IMAGE:824233 /clone_end=3'	1	AGTGGCTCTCTGCTGTTAGCATGGTT ACTAATTTGGTTACTTTCTAT
7871	db mining	Hs.320385	BF512292	11597471	UI-H-BW1-amb-d-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069359 /clone_end=3'	1	TGACCTAGTGTCACTTCAGCAGAA CCTGTGGGTATATGCCACCTCAT

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7872	db mining	Hs.105506	AA521196	2261739	aa74c04.s1 cDNA, 3' end /clone=IMAGE:826662 /clone_end=3'	1	AAGGAGAACTGTCAACTGAATCTCAA ATGCAGTCAAATGAAGAGAGGCAT
7873	db mining	Hs.124928	AA765759	2816997	oa07h05.s1 cDNA, 3' end /clone=IMAGE:1304313 /clone_end=3'	1	TTCAGTCAATTAGGTTGGCATA CAGGGTTAACCTGTGATGTACAT
7874	db mining	Hs.320488	BF513286	11598465	UI-H-BW1-amo-e-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070580 /clone_end=3'	1	AGCAGAACACATGTGTTGACACTT TTCCCTCTCTGTAATGAGGTACAT
7875	db mining	Hs.122891	AA767801	2818816	oa45h09.s1 cDNA, 3' end /clone=IMAGE:1307969 /clone_end=3'	1	TGCCCTGTGTTGGTCAAAGGAATCATC TATGCTAATGTATTGAGGCCAAT
7876	db mining	Hs.116435	AA648285	2574714	ns20d12.s1 cDNA, 3' end /clone=IMAGE:1184183 /clone_end=3'	1	ACCGAAAGCAGCATTTCATGTTA ATTAAATCGATGCAGGAAATTGTG
7877	db mining	Hs.300303	AW292760	6699396	UI-H-BW0-aij-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729453 /clone_end=3'	1	GTCCTGGCCCTTCACTCTCGTCCA GGCTCTGACCTCTTCCCTCTG
7878	db mining	Hs.123154	AA688058	2674984	nv58c04.s1 cDNA, 3' end /clone=IMAGE:1233990 /clone_end=3'	1	TGTCCGCTGTTTACCTCACTGCTCC TGTTATGCCCTTAACCTCTGCTG
7879	db mining	Hs.320489	BF513296	11598475	UI-H-BW1-amo-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070628 /clone_end=3'	1	GCACAAGACCTCACTTGGAACAGTA CCAGGCAGAACAGAGCATTACCTG
7880	db mining	Hs.124353	AA830448	2903547	oc51d05.s1 cDNA, 3' end /clone=IMAGE:1353225 /clone_end=3'	1	TTTCATATCTGGCAGTGGATGCGG TAAGGCCACAGAGAACACCACCTG
7881	db mining	Hs.122824	AA765319	2816557	oa01f11.s1 cDNA, 3' end /clone=IMAGE:1303725 /clone_end=3'	1	AGGACCCCTTCCCATAATTCTGGCT ATATACAAGGATATCCAGACACTG
7882	db mining	Hs.124317	AA827178	2901175	ob53g04.s1 cDNA, 3' end /clone=IMAGE:1335126 /clone_end=3'	1	ACCAGGCTAGAACATTAGTTCTAGG TGAAACTATTGGCCTATCAGATG
7883	db mining	Hs.300373	AW297820	6704445	UI-H-BW0-aij-h-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731230 /clone_end=3'	1	GTGCATTTAGAACAGACTTCCAGG TTCCAGCGCGGCCAGGAAGGGG
7884	db mining	Hs.320464	BF513050	11598229	UI-H-BW1-amn-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070349 /clone_end=3'	1	CTGTCATGCACCAACCTCATCCCTCC TTCAGGCCAGGGACAGTCCCTAG
7885	db mining	Hs.313366	AW297537	6704173	UI-H-BW0-ajf-f-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731160 /clone_end=3'	1	AGAGGAGGAGGGGGTAGAATGAATT TCATTTAAAGCTAACCTAGTCAG
7886	db mining	Hs.320427	BF512648	11597827	UI-H-BW1-amg-d-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069762 /clone_end=3'	1	CAGTCTCCAGCTTCTGGCCTCCT CTGCCAACCTGGATGCAAGGCTAG
7887	db mining	Hs.252840	AW015143	5863980	UI-H-Bip-abp-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2711149 /clone_end=3'	1	TGGAGAGAACGGTCGGGAAGACGAG GGGGCTGGAGGTTGGAAAGACAG
7888	db mining	Hs.313161	AW292801	6699437	UI-H-BW0-aij-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729813 /clone_end=3'	1	CTGAAATGGGGAGGTGGTTATG ACAAAAGTTCATGGAGAGGCCCTGAAG
7889	db mining	Hs.309124	AI380478	4190331	tf95a09.x1 cDNA, 3' end /clone=IMAGE:2107000 /clone_end=3'	1	TAACCGGTACGGGATTCCGCACCC TACTCCAGCAAGAACAGGCCCTGAAG
7890	db mining	Hs.120562	AA741098	2779688	ny99g07.s1 cDNA, 3' end /clone=IMAGE:1286480 /clone_end=3'	1	AGCATTCACTCTCCAAACACACTCC CAGGGTTAGGTCTTACCTCTGC
7891	db mining	Hs.105530	AA521450	2261993	aa69d11.s1 cDNA, 3' end /clone=IMAGE:826197 /clone_end=3'	1	GGTGTGAATATTATACGGATTGGC ATCATAAGATAACCGCGATAACCTGC
7892	db mining	Hs.123194	AA805997	2874747	oc18g05.s1 cDNA, 3' end /clone=IMAGE:1341272 /clone_end=3'	1	ACCTAGTCTAACTGCCTCTGTAAA GTGGGTTGCTATAGCTTTAACCC
7893	db mining	Hs.122833	AA765597	2816835	oa08a10.s1 cDNA, 3' end /clone=IMAGE:1304346 /clone_end=3'	1	TGAGGTTGGATGGTGGCAGGTAAAA CAGAAAGCAGATGTACATCTGAC
7894	db mining	Hs.313827	AW452984	6993760	UI-H-BW1-amd-g-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069525 /clone_end=3'	1	TGGAGCTGCTACATAATTTCAGG TCTCAAAGCTTCAAGAACAGTGAC
7895	db mining	Hs.122383	AA789140	2849260	aa66g10.s1 cDNA, 3' end /clone=IMAGE:825954 /clone_end=3'	1	AGACGGAACCTGAGATGTTGGATGTT GTTGATCTTAGCAAACAGACTTA
7896	db mining	Hs.120226	AA731687	2752578	nw58f05.s1 cDNA, 3' end /clone=IMAGE:1250817 /clone_end=3'	1	AGATCTGTAATCTTGGCAAATGGAA CTCACCTGCAACGATAACCTACTTA
7897	db mining	Hs.120288	AA731998	2753949	nw81b04.s1 cDNA, 3' end /clone=IMAGE:1251055 /clone_end=3'	1	GAGGACTTCATTCCCCATTCCTCGC ATACCTGCTGTTCTGTGATTA
7898	db mining	Hs.123168	AA804519	2873650	ns28a11.s1 cDNA, 3' end /clone=IMAGE:1184924 /clone_end=3'	1	AGCTCACACCTGTTCCCTCATGGGTC AGTCCCTTCATTTCACTTTGA
7899	db mining	Hs.124369	AA830835	2903934	oc54b06.s1 cDNA, 3' end /clone=IMAGE:1353491 /clone_end=3'	1	AGCTGCTGCTCTCTTCACTGGCAA ATGCAAACCTGTTATAATCTTGA

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7900	db mining	Hs.122482	AA767335	2818350	nz85h02.s1 cDNA, 3' end /clone=IMAGE:1300371 /clone_end=3'	1	TCAATATCTGTGTCCTTTCATGAGT GGCTGTACTTGTGAAGAATTGA
7901	db mining	Hs.313287	AW296059	6702695	UI-H-BW0-alu-g-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730798 /clone_end=3'	1	TGAGTGGACTGAGGAATGAATAGAAA ACGTGGATATATGTAGAAAGCTGA
7902	db mining	Hs.120705	AA748015	2787973	nx87c05.s1 cDNA, 3' end /clone=IMAGE:1269224 /clone_end=3'	1	ACCAGCCCTGGGAATGTTATGAGCA AATGATACTCCATGAGTAAATGA
7903	db mining	Hs.320495	BF513385	11598584	UI-H-BW1-amk-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070242 /clone_end=3'	1	TCGTGTGAGTGAGAGACATGTTCA TTGTGAAAAGATACTCCTAGTGG
7904	db mining	Hs.121104	AA721020	2737155	nx89f11.s1 cDNA, 3' end /clone=IMAGE:1269453 /clone_end=3'	1	TTTGTCAAATGCCTGTTCACCATCTG TGGAAGTCATTATATGATTAGGA
7905	db mining	Hs.124297	AA827809	2900172	od08c04.s1 cDNA, 3' end /clone=IMAGE:1367334 /clone_end=3'	1	ACACTTTCTCTAAGGAGAGCTTCT TAGGCATTCAAAGAACCTTCGA
7906	db mining	Hs.320372	BF512096	11597308	UI-H-BW1-arn-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070218 /clone_end=3'	1	ACCAAATGAGTACCATCTGTTGAACA CAGGGTGGCATCCAAAGTGTTC
7907	HUVEC cDNA	Hs.92381	AB007956	3413930	mRNA, chromosome 1 specific transcript KIAA0487 /cds=UNKNOWN	1	ACCTGACTTCCACGATAAAATGGAGA TGAGTCAGGGTGTAGTGTATAGT
7908	HUVEC cDNA	Hs.24950	AB008109	2554613	regulator of G-protein signalling 5 (RGS5), mRNA /cds=(81,626)	1	TGCAGATTTATACTCCTGACGTGTCT CATTACAGCTAAATAATAGGCCA
7909	HUVEC cDNA	Hs.306193	AB011087	3043553	hypothetical protein (LQFBS-1), mRNA /cds=(0,743)	1	ACCCCTGCCCTTCCCTCCGGTTAG TACCTATTGTTCTCCTTCAAAT
7910	HUVEC cDNA	Hs.154919	AB014525	3327083	mRNA for KIAA0625 protein, partial cds /cds=(0,2377)	1	AAGAGGAATGGCAGAATTAAAGCA GAAACAAGAAGATGGACATGGATT
7911	HUVEC cDNA	Hs.153026	AB014540	3327093	mRNA for KIAA0640 protein, partial cds /cds=(0,1812)	1	AAGAGTGTGTTGAGTGCCTGTCATCG GTGTTTCCCTATAAGTAGGGAT
7912	HUVEC cDNA	Hs.24439	AB014546	3327105	ring finger protein (C3HC4 type) 8 (RNFB), mRNA /cds=(112,1569)	1	CTGCTGTCCACTTCCCTCAGGCTCT GTGAATACTCAACCTGCTGTGAT
7913	HUVEC cDNA	Hs.155829	AB014576	3327165	mRNA for KIAA0876 protein, partial cds /cds=(0,3789)	1	TTCCCTGGATTCAATTCACTTGCTTA GAAATTACACTGTGCTCAATGCC
7914	HUVEC cDNA	Hs.93675	AB022718	4204189	decaludal protein induced by progesterone (DEPP), mRNA /cds=(218,856)	1	AGGTCTGCACTGCCCCCTCTCTGTG AGCTGTCAGTCTAGGTTATTCTCT
7915	HUVEC cDNA	Hs.104305	AB023143	4589483	death effector filament-forming Ced-4-like apoptosis protein (DEFCAP), transcript variant B, mRNA /cds=(522,4811)	1	GAATAGGAGGGACATGGAACCATTTG CCTCTGGCTGTGTCACAGGGTGAG
7916	HUVEC cDNA	Hs.103329	AB023187	14133226	KIAA0970 protein (KIAA0970), mRNA /cds=(334,2687)	1	CCTGTTAAGAAAGTGAATGTTATG GTCTCCCTCTTCAATGAGCTTA
7917	HUVEC cDNA	Hs.155182	AB028959	5689408	KIAA1036 protein (KIAA1036), mRNA /cds=(385,1482)	1	TTTCACTTTCACACTTCATCTATTCC TGTGTCACTTCCCGAACAGA
7918	HUVEC cDNA	Hs.129216	AB028997	5689484	DNA sequence from clone RP11-145E8 on chromosome 10. Contains the gene KIAA1074, the 3' end of the YME1L1 gene for YME1 (<i>S.cerevisiae</i>)-like 1, ESTs, STSs, GSs and a CpG island /cds=(166,5298)	1	TCTGGATCAATAGCTCCCTCTAGG GTCTACTGTGAGTCAGAACATCTAA
7919	HUVEC cDNA	Hs.8383	AB032255	6683499	bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA /cds=(366,6284)	1	TTTATCTACTGTGTTGTTGGTGGCC TTGTTGGAGGCAATAGATCAGATT
7920	HUVEC cDNA	Hs.15165	AB037755	7243048	novel retinal pigment epithelial gene (NORPEG), mRNA /cds=(111,3053)	1	GACATTTTGAGGATGCCTGACGAG GTGTAGCCTTTATCTGTTCCG
7921	HUVEC cDNA	Hs.82113	AB049113	10257384	dUTP pyrophosphatase (DUT), mRNA /cds=(29,523)	1	CCCAGTTGAGGACACAGCAGAACAG AGTGTCTTTCTGGTGAATTCTCCA
7922	HUVEC cDNA	Hs.8180	AF000652	2785862	syndecan binding protein (syntenin) (SDCBP), mRNA /cds=(148,1044)	1	TGTCCTTCTCTGACTCTCTCTTG AACACAAATGATAGTTGACACTTT
7923	HUVEC cDNA	Hs.147916	AF000982	2580549	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 (DDX3), transcript variant 2, mRNA /cds=(856,2844)	1	GTGACTTGTACATTCAAGCAATAGCAT TTGAGCAAGTTTATCAGCAAGCA
7924	HUVEC cDNA	Hs.75056	AF002163	2290769	adaptor-related protein complex 3, delta 1 subunit (AP3D1), mRNA /cds=(209,3547)	1	TTGCTATCGACATTCCCGTATAAAGA GAGAGACATATCACGCTGCTGTCA
7925	HUVEC cDNA	Hs.42915	AF006082	2282029	ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA /cds=(74,1258)	1	CCTGCCAGTGTCAAGAAAATCTTATT ATGAATCCTGTCGGTATTCTTGG
7926	HUVEC cDNA	Hs.11538	AF006084	2282033	actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1B), mRNA /cds=(80,1198)	1	AGGGAGGGACAGATGGGGAGCTT TCTTACCTTCAAGGAATACGTGC
7927	HUVEC cDNA	Hs.6895	AF006086	2282037	actin related protein 2/3 complex, subunit 3 (21 kD) (ARPC3), mRNA /cds=(25,581)	1	TCAAGAATTGGGTGGGAGAAAAGAA AGTGGGTTCAAGGGTGATTGAA
7928	HUVEC cDNA	Hs.286027	AF010313	6468761	etoposide-induced mRNA (PIG8), mRNA /cds=(72,1151)	1	TGTGATTAGTTGTTTCTGTCAATT TTGAGAGACTAAAATTGTGGGG

Table 8

7929	HUVEC cDNA	Hs.79150	AF026291	2559007	chaperonin containing TCP1, subunit 4 (delta) (CCT4), mRNA /cds=(0,1619)	1	TGGGCTTGGTCTTCCAGTTGGCATT GCCTGAAGTTGATTGAAACAAATT
7930	HUVEC cDNA	Hs.81452	AF030555	3158350	fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA /cds=(508,2641)	1	AACAAGATGAGAACAGATAAAGATTG TGTGGTGTGTTGGATTGGAGAGA
7931	HUVEC cDNA	Hs.139851	AF035752	2665791	caveolin 2 (CAV2), mRNA /cds=(20,930)	1	TGTAGCTCCCACAAGGTAAACTTCAT TGTAAGATTGCACTGTTCTGATT
7932	HUVEC cDNA	Hs.194709	AF037364	14030860	paraneoplastic antigen MA1 (PNMA1), mRNA /cds=(664,1725)	1	TCACTCCCCATTTCACTTCTTCATCC GAGAATAGTTCTTGTCTACATCG
7933	HUVEC cDNA	Hs.79516	AF039658	2773159	brain acid-soluble protein 1 (BASP1), mRNA /cds=(52,735)	1	TGGGAGTGACAAACATTCTCATCC TACTTAGCTACCTAGATTTCTCA
7934	HUVEC cDNA	Hs.29417	AF039942	4730928	HCF-binding transcription factor Zhangfei (ZF), mRNA /cds=(457,1275)	1	AATGGAAAGGATTAGTATGGCTATT TTAAAGCTGCTTGTAGGTCTCT
7935	HUVEC cDNA	Hs.26232	AF044414	6136293	mannosidase, alpha, class 2C, member 1 (MAN2C1), mRNA /cds=(56,3244)	1	CCCCAGCCTAAAGCAGGGATCAGTC TTTCTGTGAAATAATCCTTGA
7936	HUVEC cDNA	Hs.3776	AF062072	3668065	zinc finger protein 216 (ZNF216), mRNA /cds=(288,929)	1	TGTGGTAATGCCGTGTTTCATCTGTA AATAGTTAAGTATGTACACGAGGC
7937	HUVEC cDNA	Hs.74034	AF070648	3283922	clone 24651 mRNA sequence /cds=UNKNOWN	1	AGATGCTTAGTCCTCATGCAAATCA ATTACTGGTCCAAAAGATTGCTGA
7938	HUVEC cDNA	Hs.274230	AF074331	5052074	PAPS synthetase-2 (PAPSS2) mRNA, complete cds /cds=(63,1907)	1	AAAATGCTCTCTGCTTAGTACCA TGCTTAGTGCAAATGATTATTCT
7939	HUVEC cDNA	Hs.12540	AF081281	3415122	lysophospholipase I (LYPLA1), mRNA /cds=(35,727)	1	AGCTTATTAGGATCTCAACCCAGGTA ACAGGAAATAATTCTGTGGTTTCAT
7940	HUVEC cDNA	Hs.159629	AF092131	5138911	myostatin XB (MYO9B), mRNA /cds=(0,6068)	1	TCCTCGCTCTATCCATGTGGAATGCT GGACAATAAGCGAGTGCTGCCA
7941	HUVEC cDNA	Hs.273385	AF105253	7532779	guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1 (GNAS1), mRNA /cds=(68,1252)	1	GCCACACAAAGTCCCCTCACTTCA GTAAAAATAATAAAACAGCAGCA
7942	HUVEC cDNA	Hs.2934	AF107045	5006419	ribonucleotide reductase M1 polypeptide (RRM1), mRNA /cds=(187,2565)	1	ACTGCTTGACTGGTGGGCTCTAGA AGCAAAACTGAGTGATAACTCATG
7943	HUVEC cDNA	Hs.158237	AF112345	6650627	integrin alpha 10 subunit (ITGA10), mRNA, complete cds /cds=(76,3579)	1	GGCATTGTCTGTGTTCCCAGTGGGG TGGACAGTATATCAGATGGTCAGA
7944	HUVEC cDNA	Hs.183698	AF116627	7959755	ribosomal protein L29 (RPL29), mRNA /cds=(29,508)	1	CCCTGGGCTTACCATCTGCATGGGGC TGGGGTCCCTGTGCTATTGTTAC
7945	HUVEC cDNA	Hs.2186	AF119850	7770136	Homo sapiens, eukaryotic translation elongation factor 1 gamma, clone MGC:4501 IMAGE:2964623, mRNA, complete cds /cds=(2278,3231)	1	TCAAGTGAACATCTTGCACATCACC TAGCTGCCTGCACCTGCACCTTCAG
7946	HUVEC cDNA	Hs.22900	AF134891	7381111	nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA /cds=(492,1694)	1	TCTTGGCAGCCATCCTTTAAAGAGT AAGTTGGTACTTCAAAAGAGCA
7947	HUVEC cDNA	Hs.108258	AF141968	6273777	actin cross-linking factor (ACF7), transcript variant 1, mRNA /cds=(51,18343)	1	AGCTAAAGAGAGGGAACCTCATCTAA GTAACATTGACATGATAACAGCA
7948	HUVEC cDNA	Hs.11156	AF151072	7106865	hypothetical protein (LOC51255), mRNA /cds=(0,461)	1	GCTGAGTGCTGGCCCTCTGCCTCTT CCTTATTAAACCTTGAAATCCTCATTA
7949	HUVEC cDNA	Hs.179573	AF193556	6907041	collagen, type I, alpha 2 (COL1A2), mRNA /cds=(139,4239)	1	TGAATGATCAGAACTGACATTAAATTC ATGTTTGCTCGCCATGCTTCTT
7950	HUVEC cDNA	Hs.41135	AF205940	8547214	endomucin-2 (LOC51705), mRNA /cds=(78,863)	1	TCCGGGCCAAGAAATTTTATCCATGA AGACTTCTACTTTCTCGGTGT
7951	HUVEC cDNA	Hs.142908	AF219119	7158848	E2F-like protein (LOC51270), mRNA /cds=(278,979)	1	GCAGAGTTATTGTTGCCCTTAACA GTTTTCTGAGTTACTGAAGAA
7952	HUVEC cDNA	Hs.154721	AF261088	9802307	aconitase 1, soluble (ACO1), mRNA /cds=(107,2776)	1	TTATCAAGCAGAGACCTTTGGGGA GGCGGTTGGGAGAACACATTCT
7953	HUVEC cDNA	Hs.76288	AF261089	9802309	calpain 2, (m/l) large subunit (CAPN2), mRNA /cds=(142,2244)	1	GGGTATGCTGCCCTGTAAATTCTATG TATTCAAAGGAAAAGACACCTTC
7954	HUVEC cDNA	Hs.152707	AJ001259	2769253	glioblastoma amplified sequence (GBAS), mRNA /cds=(8,868)	1	TTGCTGCCCTCACATCAAGAATGTA TGTGAAAGTGTGAAATAATCTCA
7955	HUVEC cDNA	Hs.5097	AJ002308	2959871	synaptotagmin 2 (SYNGR2), mRNA /cds=(29,703)	1	ATGCCCGGCCCTGGATGCTTTG AGACGGAATAATGTTCTCATTC
7956	HUVEC cDNA	Hs.143323	AJ243706	6572290	mRNA for RB-binding protein (rbbp2h1a gene) /cds=(757,5802)	1	ACGAGTTGTGATATAGCAGAGGTTT AAATGTACCCCTCCCTTTATGCA
7957	HUVEC cDNA	Hs.1197	NM_002157	4504522	Heat shock 10kD protein 1 (chaperonin 10)	1	TGATGCTGCCATTCCACTGAAGTTC TGAAATCTTCGTATGTAAATAA
7958	HUVEC cDNA	Hs.79037	BC010112	14603308	Homo sapiens, heat shock 60kD protein 1 (chaperonin), clone MGC:19755 IMAGE:3630225, mRNA, complete cds /cds=(1705,3396)	1	AGCACGCCTTCTGTGGAGAGTGGAGAA TAATTGTGTACAAAGTAGAGAAGT
7959	HUVEC cDNA	Hs.279860	AJ400717	7573518	tumor protein, translationally-controlled 1 (TP1), mRNA /cds=(94,612)	1	CATCTGAAGTGTGGAGCCTTACCCAT TTCATCACCTACAACGGAAGTAGT

Table 8

7860	HUVEC cDNA	Hs.165563	AK024508	10440535	DNA sequence from clone RP4-591C20 on chromosome 20. Contains ESTs, STSs, GSSs and CpG islands. Contains a novel gene for a protein similar to NG26, the TPD52L2 gene for two isoforms of tumor protein D52-like protein 2, a gene for a novel Dnaj domain protein similar to mouse and bovine cysteine string protein with two isoforms, a gene for a novel phosphoributokinase with three isoforms, the KIAA1196 gene and the 5' part of the TOM gene for a putative mitochondrial outer membrane protein import receptor similar to yeast pre-mRNA splicing factors Prp1/Zer1 and Prp6 /cds=(0,503)	1	GCCAGGCTGGTTCGCATGGTGATC TCCGTCTGTATGTCTGAATGTTGG
7861	HUVEC cDNA	Hs.91146	AL050147	4884153	protein kinase D2 mRNA, complete cds /cds=(39,2675)	1	CTATTCCAAGGCCCTCCCTGTTTC CCAGCAATTAAACGGACTCATC
7862	HUVEC cDNA	Hs.66762	AL050367	4914600	mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026) /cds=UNKNOWN	1	AAAGTGCAGAACATGACTCTTCGTGC ATTCTTCTAAAGAGCTGCTTGGT
7863	HUVEC cDNA	Hs.165998	AL080119	5262550	PAI-1 mRNA-binding protein (PAI-RBP1), mRNA /cds=(85,1248)	1	TTGTTGGTAGGCACATCGTCAAGT GAAGTAGTTTATAGGTATGGGTT
7864	HUVEC cDNA	Hs.111801	AL096723	5419856	mRNA; cDNA DKFZp564H2023 (from clone DKFZp564H2023) /cds=UNKNOWN	1	AGTCTGTATCATCCATACTTGTACTA CCTTGTCCATGAAGCTGAGA
7865	HUVEC cDNA	Hs.89434	AL110225	5817161	drebrin 1 (DBN1), mRNA /cds=(97,2046)	1	TTGCCCGCTTCCCTACCCACAGGGC CTGACTTTTACAGCTTTCTTTT
7866	HUVEC cDNA	Hs.7527	AL110239	5817182	small fragment nuclease (DKFZP566E144), mRNA /cds=(77,790)	1	TATGACACAGCAGCTCCTTGTAAAGT ACCAAGTCATGTCCATCCCTTGGT
7867	HUVEC cDNA	Hs.187991	AL110269	5817043	DKFZP564A122 protein (DKFZP564A122), mRNA /cds=(2570,2908)	1	TTGGTAGTTGCCAAAGAACAAATAC AGCATATCTCTTTGCCTTCTGT
7868	HUVEC cDNA	Hs.25882	AL117665	5912262	mRNA; cDNA DKFZp586M1824 (from clone DKFZp586M1824); partial cds /cds=(0,3671)	1	TGCAAGATGACCTTGGATTATTGG ACTCTGACTATTGGGACCCCAAAT
7869	HUVEC cDNA	Hs.17428	AL133010	6453416	RBP1-like protein (BCAA), transcript variant 2, mRNA /cds=(466,4143)	1	TGGACGCCCTAACAAACAGAGAAAAC AGAAATAAACACAGGAACGTCTT
7870	HUVEC cDNA	Hs.278242	AL137300	6807762	Homo sapiens, clone MGC:3214 IMAGE:3502620, mRNA, complete cds /cds=(2066,3421)	1	CAATAGCTTGTGGGTCTGTGAAGACT GGGGTGTGTTGAGTTCTCACACCC
7871	HUVEC cDNA	Hs.7378	AL137663	6807784	mRNA; cDNA DKFZp434G227 (from clone DKFZp434G227) /cds=UNKNOWN	1	TGCACTGTACTCTCATAGGATTG TAAAGGTGTTCTAATCCAATTGCA
7872	HUVEC cDNA	Hs.61289	AL157424	7018453	mRNA; cDNA DKFZp761E1512 (from clone DKFZp761E1512) /cds=UNKNOWN	1	TGAAGTCATTCTATTGGAGGAAAG CTGCAAGATTATTGGGGACTAG
7873	HUVEC cDNA	Hs.240013	AL390148	9368882	mRNA; cDNA DKFZp547A166 (from clone DKFZp547A166) /cds=UNKNOWN	1	TTTCATCTGGCCCACCCCTCCTAGAC TCTCCTCCCTCAAGAGTTGGAGC
7874	HUVEC cDNA	Hs.22629	AW887820	8049833	602281231F1 cDNA, 5' end /clone=IMAGE:4368943 /clone_end=5'	1	GTGAGAATTGGATCCAGTCATCTC ACAGAACCTTCACTAGGGTGC
7875	HUVEC cDNA	Hs.333414	BE562833	9806553	hypothetical protein MGC14151 (MGC14151), mRNA /cds=(108,485)	1	CGGACCCCAGTTCTTGATCCAAGGG GGAAAGATGCGGGGACCCAAATGG
7876	HUVEC cDNA	NA	BE612847	9894444	601452239F1 NIH_MGC_66 cDNA clone IMAGE:3856304 5', mRNA sequence	1	TAAAGATGTCCGGGTACACTTCGCCA AGGGTTAGCGTCTTGGCATTTC
7877	HUVEC cDNA	Hs.86412	BE876332	10325018	chromosome 9 open reading frame 5 (C9orf5), mRNA /cds=(32,2767)	1	AACACAACACTAAAACCGAACACACA CGTACTAACACACCCACGACCAA
7878	HUVEC cDNA	Hs.285814	BE905669	10400012	sprouty (Drosophila) homolog 4 (SPRY4), mRNA /cds=(205,525)	1	CCTCTGGTTCTGCTTTGACAGCA TTTTGTGCCCCCTCTGTACTGTG
7879	HUVEC cDNA	Hs.113029	BF025727	10733439	ribosomal protein S25 (RPS25), mRNA /cds=(63,440)	1	GATATACGAAACACACACTGGACGA TGCAGAAAACGAGACGACATAAGC
7880	HUVEC cDNA	Hs.263339	BF107006	10889631	602377929F1 cDNA, 5' end /clone=IMAGE:4508646 /clone_end=5'	1	TGGACAGGCATGAAAGGTTACAATG GGAGAAAACACACACGTTATGT
7881	HUVEC cDNA	Hs.182426	BF204683	11098269	601867521F1 cDNA, 5' end /clone=IMAGE:4110052 /clone_end=5'	1	GCAGGAGAGCGAGAGAGGAGAAAGAA GAGGCAGGAGGGAGAAAGAGCGTAC
7882	HUVEC cDNA	Hs.75968	BF217687	11111273	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(77,211)	1	CAAGAACGAGAACAGCAGAACACA ACAGAGAGACAAACGAGAACACA
7883	HUVEC cDNA	Hs.112318	BF237710	11151628	cDNA FLJ14633 fis, clone NT2RP2000938 /cds=UNKNOWN	1	AGAGGAAAGAATAGGACCAGTGGCG AGGTATAGGGAGGGAGGGCATACTAA
7884	HUVEC cDNA	Hs.293981	BF247088	11162147	Homo sapiens, clone MGC:16393 IMAGE:3939021, mRNA, complete cds /cds=(506,1900)	1	TCGGAGTAAGGGCGATTGTCTCGTA GGTAATACATCATCTTCGTGCATA

Table 8

7985	HUVEC cDNA	Hs.157850	BF303931	11250608	Homo sapiens, clone MGC:15545 IMAGE:3050745, mRNA, complete cds /cds=(1045,1623)	1	AGACAAGACGAGCAACGACAACCAC AGCAGCTCCATACACTCTGCCCTCTC
7986	HUVEC cDNA	Hs.217493	D00017	219909	annexin A2 (ANXA2), mRNA /cds=(49,1068)	1	AGTGAAGTCTATGATGTAAACACTT TGCCCTCTGTACTGTGTCTATAA
7987	HUVEC cDNA	Hs.76549	D00099	219941	mRNA for Na,K-ATPase alpha-subunit, complete cds /cds=(318,3389)	1	TCACAAGACGTCTCATCGAACAGTA AATATCCGCTGCCAGTTCGATCA
7988	HUVEC cDNA	Hs.330716	D10522	219893	cDNA FLJ14368 fis, clone HEMBA1001122 /cds=UNKNOWN	1	AAACTCCTGCTTAAGGTGTTCTAAATT TCTGTGAGCACACTAAAAGCGAA
7989	HUVEC cDNA	Hs.75929	D21255	575578	mRNA for OB-cadherin-2, complete cds /cds=(476,2557)	1	CGTGCAGATATAACTGTCTGTTTC AGTGAGAGACGCCCTATTCTATG
7990	HUVEC cDNA	Hs.178710	D21260	434760	clathrin, heavy polypeptide (Hc) (CLTC), mRNA /cds=(172,5199)	1	TCCCTGAGGCTTGTATGTTGGATA TTGTGGTGTGTTAGATCACTGAGT
7991	HUVEC cDNA	Hs.334822	D23660	432358	Homo sapiens, Similar to ribosomal protein L4, clone MGC:2668 IMAGE:3139805, mRNA, complete cds /cds=(1616,2617)	1	CAGAGAAGAAACCTACTACAGAGGA GAAGAACGCTGCTGCATCAAACCTCTT
7992	HUVEC cDNA	Hs.262823	D28500	7678803	hypothetical protein FLJ10326 (FLJ10326), mRNA /cds=(2,2296)	1	TCAGAACATAGATATGTATTGAGCTT GTCTTCAAATACGGCCAAGCAGAA
7993	HUVEC cDNA	Hs.151761	D43947	603948	KIAA0100 gene product (KIAA0100), mRNA /cds=(329,6607)	1	TTGGGGTCAAGTGAAAGGGTAGGGG GATAGCTCTGATCAAGTGTGATAAA
7994	HUVEC cDNA	Hs.699	D50525	1167502	peptidylprolyl isomerase B (cyclophilin B) (PPIB), mRNA /cds=(21,671)	1	CAGCAAATCCATCTGAACGTGGAGG AGAAGCTCTTTACTGAGGGTGC
7995	HUVEC cDNA	Hs.278607	D50911	6633996	mRNA; cDNA DKFZp434N0735 (from clone DKFZp434N0735); partial cds /cds=(0,1577)	1	CCTCTCTCATGTGTGAAATCTGTA ATATACCAATTCTGTGGCTGT
7996	HUVEC cDNA	Hs.57729	D50922	1469186	Kelch-like ECH-associated protein 1 (KIAA0132), mRNA /cds=(112,1986)	1	GGATGGCACTTCCCCACCGGATGGA CAGTTATTGTTGATAAGTAACCC
7997	HUVEC cDNA	Hs.240770	D59253	1060898	Homo sapiens, nuclear cap binding protein subunit 2, 20kD, clone MGC:4991 IMAGE:3458927, mRNA, complete cds /cds=(26,496)	1	TGAGTCAGTGTCTTACTGAGCTGGA AGCCTCTGAAAGTTATTAAAGGCA
7998	HUVEC cDNA	Hs.155595	D63878	961447	neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(258,1343)	1	CCACACACTGCTACACTCTGATCCCC TTTGGTTTTACTACCCAAATCTAA
7999	HUVEC cDNA	Hs.80712	D86957	1503987	septin 2 (SEP2) mRNA, partial cds /cds=(0,1527)	1	GTCGGTTGCTAGTCTGTTACGTTAAC ATGCTTTCTAAATTGCTTCACG
8000	HUVEC cDNA	Hs.75822	D86970	1504013	mRNA for KIAA0216 gene, complete cds /cds=(484,5229)	1	TTGTAACACTGGCTGTGCTCTCCC CTGTTACCGATGTATGGAATAA
8001	HUVEC cDNA	Hs.170311	D89678	3218539	heterogeneous nuclear ribonucleoprotein D-like (HNRPD), transcript variant 1, mRNA /cds=(580,1842)	1	TTTATGATTAGGTGACGAGTTGACAT TGAGATTGCTCTTCCCCTGATC
8002	HUVEC cDNA	Hs.83213	J02874	178346	fatty acid binding protein 4, adipocyte (FABP4), mRNA /cds=(47,445)	1	TTGTTGTTTCCCTGATTAGCAAGCA AGTAATTCTCCAAAGCTTCTCT
8003	HUVEC cDNA	Hs.177766	J03473	337423	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) (ADPRT), mRNA /cds=(159,3203)	1	TTAGAAACAAAAAGAGCTTCTCT CCAAGAAACTGAACATGGGAGCT
8004	HUVEC cDNA	Hs.155560	L10284	186522	calnexin (CANX), mRNA /cds=(89,1867)	1	CCATTGTTGCAATGCCAGTGTCC ATCAGATGTTCTCCATTCTCT
8005	HUVEC cDNA	Hs.75693	L13977	431320	prolylcarboxypeptidase (angiotensinase C) (PRCP), mRNA /cds=(29,1519)	1	GATGTCGGTGCCTAACATCCCAGGAA GTGAGAGCCATTCTTTGTACTGG
8006	HUVEC cDNA	Hs.539	L31610	1220360	ribosomal protein S29 (RPS29), mRNA /cds=(30,200)	1	AGTTGGACTAAATGCTTCCCTCAG AGGATTATCCGGGGCATCTACTCA
8007	HUVEC cDNA	Hs.1742	L33075	536843	IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA /cds=(467,5440)	1	TGAATTACTTCTCCCAAAGAGTTTG GACTGCCCGTCAGATTGTTCTGC
8008	HUVEC cDNA	Hs.180446	L38951	893287	importin beta subunit mRNA, complete cds /cds=(337,2967)	1	AAACACATACACACAAAACAGCAAC TTCAAGGTAACCTATTGGATTGCA
8009	HUVEC cDNA	Hs.79572	M11233	181179	cathepsin D (lysosomal aspartyl protease) (CTSD), mRNA /cds=(2,1240)	1	CTGAGGATGAGCTGGAGGAGTGAG AGGGGACAAACCCACCTTGTGGA
8010	HUVEC cDNA	Hs.273415	M11560	178350	aldolase A, fructose-bisphosphate (ALDOA), mRNA /cds=(167,1261)	1	TCTTCTCCCTGGTACAGTGGTGT GTGGTGTGCTGTGAATGCTAAG
8011	HUVEC cDNA	Hs.254105	M14328	182113	enolase 1, (alpha) (ENO1), mRNA /cds=(94,1398)	1	GCTAGATCCCCGGTGGTTTGTGCTC AAAATAAAAAGCCTCAGTGACCCA
8012	HUVEC cDNA	Hs.237519	M20867	183059	yz35c09.s1 cDNA, 3' end /clone=IMAGE:285040 /clone_end=3'	1	GCATGGCTTAACCTGGTGATAAAAGC AGTTATTAAAAGTCTACGTTTCC
8013	HUVEC cDNA	Hs.1239	M22324	178535	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150) (ANPEP), mRNA /cds=(120,3023)	1	CCGCCCTGTACCTCTTACCTTCC CCTAAAGACCTAAATCTGAGGAA
8014	HUVEC cDNA	Hs.118126	M22960	190282	protective protein for beta-galactosidase (galactosialidosis) (PPGB), mRNA /cds=(6,1448)	1	GGACAGCCCACAGGGAGGTGGTGA CGGACTGTAATTGATAGATTGATTA
8015	HUVEC cDNA	Hs.198281	M26252	338826	pyruvate kinase, muscle (PKM2), mRNA /cds=(109,1704)	1	ATTGAAGCCGACTCTGGCCCTGGCC CTTACTTGCTCTAGCTCTAG

Table 8

8016	HUVEC cDNA	Hs.2050	M31166	339991	pentaxin-related gene, rapidly induced by IL-1 beta (PTX3), mRNA /cds=(67,1212)	1	ACTAGACTTATGCCATGGTGCCTTC AGTTAAATGCTGTCTCTGTCAG
8017	HUVEC cDNA	Hs.99853	M59849	182591	fibrillarin (FBL), mRNA /cds=(59,1024)	1	GAGCCATATGAAAGAGACCATGCCGT GGCGTGGGAGTGTACAGGCCACC
8018	HUVEC cDNA	Hs.283473	M64098	183891	hypothetical protein PRO2900 (PRO2900), mRNA /cds=(271,501)	1	ATAACAGACTCCAGCTCCTGGTCCAC CGGGCATGTCACTGCACACTCTGG
8019	HUVEC cDNA	Hs.211573	M85289	184426	heparan sulfate proteoglycan 2 (perlecan) (HSPG2), mRNA /cds=(40,13221)	1	CTGGCCTCTGTGTCCTAGAAGGGAC CCTCCTGTGCTTTGTCTTGATT
8020	HUVEC cDNA	Hs.75103	M86400	189952	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), mRNA /cds=(84,821)	1	CCCAAAGCTCACTTACAAATATTTC CTCAGTACTTGCAGAAAACACCC
8021	HUVEC cDNA	Hs.59271	M96982	338262	U2(RNU2) small nuclear RNA auxiliary factor 1 (non-standard symbol) (U2AF1), mRNA /cds=(38,760)	1	ATGTCTGCTAGAAAGTGGTAGTTG ATTGACCAAAACAGTTCATAAAGGG
8022	HUVEC cDNA	Hs.110802	NM_000552	9257255	von Willebrand factor (VWF), mRNA /cds=(310,8751)	1	CTCTGCATGTTCTGCTTGTGCCCT TCTGAGCCCACAATAAAGGCTGAG
8023	HUVEC cDNA	Hs.274466	NM_001403	4503472	eukaryotic translation elongation factor 1 alpha 1-like 4 (EEF1A1L14), mRNA /cds=(620,1816)	1	TGCATCGAAAACCTTCAAGAGGAA AGGAGAACATTTGTGGACACGTT
8024	HUVEC cDNA	Hs.279518	NM_001642	4502146	amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA /cds=(72,2363)	1	AGCCCTATTCAATGCTCTACCCACTA TGCACAGATTAAACCTCACCTACA
8025	HUVEC cDNA	Hs.76224	NM_004105	9665261	EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 1, mRNA /cds=(149,1630)	1	AGTGACAGTGAACTTAAGCAAATTAC CCTCCTACCCATTCTATGGAATA
8026	HUVEC cDNA	Hs.19545	NM_012193	6912383	frizzled (Drosophila) homolog 4 (FZD4), mRNA /cds=(306,1919)	1	ACACATGCCCTGAATGAATTGCTAA TTTCAAAGGAAATGGACCTGCTT
8027	HUVEC cDNA	Hs.87125	NM_014600	7657055	EH-domain containing 3 (EHD3), mRNA /cds=(285,1892)	1	GCCACTGAACCAATCACTTTGTATGC TATGCTCTACTGTGATGGAAAAC
8028	HUVEC cDNA	Hs.119503	NM_016091	7705432	HSPC025 (HSPC025), mRNA /cds=(33,1727)	1	AGGACCGAAGTGTTCAGTGGATCT CAGTAAAGGATCTTGGAGCCAGA
8029	HUVEC cDNA	Hs.7905	NM_016224	7706705	SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA /cds=(43,1830)	1	TTCATGGAAAAATGAGGGGTTCTCC CCACTGATATTTACATAGACTCA
8030	HUVEC cDNA	Hs.283722	NM_020151	9910251	GTT1 protein (GTT1), mRNA /cds=(553,1440)	1	GCTCCATGTTCTGACTTAGGCAATT TGATTCCTGCACTGGGGCTGTCT
8031	HUVEC cDNA	Hs.286233	NM_020414	14251213	sperm autoantigenic protein 17 (SPA17), mRNA /cds=(1210,1665)	1	GCAGCAGCTTAATTTCCTGTATTGC AGTGTATAGCCTCTGTGTGT
8032	HUVEC cDNA	Hs.272822	S56985	298485	RuvB (E coli homolog)-like 1 (RUVBL1), mRNA /cds=(76,1446)	1	ACCTCCCACITGTCTGTACATACTG GCCTCTGTGATTACATAGATCAGC
8033	HUVEC cDNA	Hs.279518	S60099	300168	amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA /cds=(72,2363)	1	AGCCCTATTCAATGCTCTACCCACTA TGCACAGATTAAACCTCACCTACA
8034	HUVEC cDNA	Hs.194662	S80562	1245968	calponin 3, acidic (CNN3), mRNA /cds=(83,1072)	1	ACATGAAAGACTAAACTCATGCTTAT TGCTAAATGTGGCTTTGCCAACT
8035	HUVEC cDNA	Hs.76669	U08021	494988	nicotinamide N-methyltransferase (NNMT), mRNA /cds=(117,911)	1	AGACCCCTGTGATGCCCTGTGACCTCA ATAAAGCAATTCTTGACCTGT
8036	HUVEC cDNA	Hs.89657	U13991	562076	TATA box binding protein (TBP)-associated factor, RNA polymerase II, H, 30kD (TAF2H), mRNA /cds=(17,673)	1	CGCACTACTTACCTGAGCCCCCAA CCTAAATGTACTTATCTGTCCCCA
8037	HUVEC cDNA	Hs.1516	U20982	695253	insulin-like growth factor binding protein-4 (IGFBP4) gene, promoter and complete	1	CTGTAGACTCAGTGCAGCCACAGCT TCAGAGATTGTGCTCACATGGTAT
8038	HUVEC cDNA	Hs.183648	U22816	930342	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (iprin), alpha 1 (PPFIA1), mRNA /cds=(229,3837)	1	TGACAAAGGATTTACGTTATAAAAT TATGACAGAAGCCATGTGCCCCG
8039	HUVEC cDNA	Hs.83383	U25182	799380	thioredoxin peroxidase (antioxidant enzyme) (AOE372), mRNA /cds=(43,858)	1	GTCTGCCCTGCTGGCTGGAAACCTG GTAGTGAACAAATAATCCAGATCC
8040	HUVEC cDNA	Hs.75888	U30255	984324	phosphogluconate dehydrogenase (PGD), mRNA /cds=(6,1457)	1	CTCGTCATACAATGCCATGGGCTC CTGTCACCCCTCACGTCTCCACAG
8041	HUVEC cDNA	Hs.169476	U34995	1497857	Homo sapiens, glyceraldehyde-3-phosphate dehydrogenase, clone MGC:10826 IMAGE:3628129, mRNA, complete cds /cds=(2306,3313)	1	CTAGGGAGCCGCACCTTATCATGTAC CATCAATAAAAGTACCCCTGTGCTCA
8042	HUVEC cDNA	Hs.192023	U39067	1718194	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) (EIF3S2), mRNA /cds=(17,894)	1	TCCGTATCCATTACTTCGACCCACAG TACTTTGAATTGAGTTGAGGCT
8043	HUVEC cDNA	Hs.155637	U47077	13570016	DNA-dependent protein kinase catalytic subunit (DNA-PKcs) mRNA, complete cds /cds=(57,12443)	1	CCAGTCCTCCACACCCAAACTGTTTC TGATGGCTTTAGCTTTGTGTT
8044	HUVEC cDNA	Hs.285313	U51869	2745959	core promoter element binding protein (COPEB), mRNA /cds=(117,988)	1	CTGTTGCTCTGTGAGGCTGCCAGTT GTTGTGTTACCGATGCCAGAAG

Table 8

8045	HUVEC cDNA	Hs.184270	U56637	1336098	capping protein (actin filament) muscle Z-line, alpha 1 (CAPZA1), mRNA /cds=(0,860)	1	AATATAGTCAGCAAGGTTGTCAG GTGACCCATTGAGCTGTATGCA
8046	HUVEC cDNA	Hs.75064	U61234	1465773	tubulin-specific chaperone c (TBCC), mRNA /cds=(23,1063)	1	TTTGCATTTCGTCATGCCCTTGAGA CTGAGTCTTACTCCGCCCCCAG
8047	HUVEC cDNA	Hs.183684	U73824	1857236	eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), mRNA /cds=(306,3029)	1	TTGGGGTGTGAAACAAATGGTGAGA ATTTGAATGGTCCCTCCTATTAT
8048	HUVEC cDNA	Hs.165263	U89278	1877500	early development regulator 2 (homolog of polyhomeotic 2) (EDR2), mRNA /cds=(8,1309)	1	CAGGAAGGAGGTAGGCACCTTCTG AGCTTATTCTATTCCCCACCCACAC
8049	HUVEC cDNA	Hs.334703	W29012	1308969	Homo sapiens, clone IMAGE:3875338, mRNA, partial cds /cds=(0,930)	1	GGGAGCCATCCCTCTCACCAAGGT GGCAATGATGGAGGGAACTTCGATG
8050	HUVEC cDNA	Hs.287820	X02761	31396	mRNA for fibronectin (FN precursor) /cds=(0,6987)	1	TGGCCCGCAACTCTGTAGGAACAAG CATGATCTTGTACTGTGATATTTC
8051	HUVEC cDNA	Hs.14376	X04098	28338	actin, gamma 1 (ACTG1), mRNA /cds=(74,1201)	1	GTTTTCTACTGTTATGTGAGAACAC AGGCCCCAGCAACACGTATTG
8052	HUVEC cDNA	Hs.290070	X04412	35447	gelsolin (amyloidosis, Finnish type) (GSN), mRNA /cds=(14,2362)	1	AGCCCTGAAAAATTAGAGTCCTTG CAAATTGCTAAAATGTCAGTGT
8053	HUVEC cDNA	Hs.79086	X06323	34753	mitochondrial ribosomal protein L3 (MRPL3), mRNA /cds=(76,1122)	1	TGGGGACTATAGTCACCTATTG GTAAGAAACCATTTGCTAAATG
8054	HUVEC cDNA	Hs.287797	X07979	31441	mRNA for FLJ00043 protein, partial cds /cds=(0,4248)	1	ACCACTGTATGTTACTTCTCACCATT TGAATTGCCATCTGTTTACA
8055	HUVEC cDNA	Hs.87409	X14787	37464	thrombospondin 1 (THBS1), mRNA /cds=(111,3623)	1	TTGACCTCCCATTTTACTATTG CAATACCTTTCTAGGAATGTGCT
8056	HUVEC cDNA	Hs.82202	X53777	34198	ribosomal protein L17 (RPL17), mRNA /cds=(286,840)	1	GAGGAGGTTGCCAGAAGAAAAAGA TATCCCAGAAGAAACTGAAGAAACA
8057	HUVEC cDNA	Hs.233936	X54304	34755	myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(114,629)	1	ACACTTACAGCCCTTCTCCCCCAATA ACTGTGGGTCTATACAGAGTCAT
8058	HUVEC cDNA	Hs.74405	X57347	32463	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YVHAQ), mRNA /cds=(100,837)	1	AGAGAGTTGGACCCTATTG GCTAATCATTGACTGTAGTCCCAA
8059	HUVEC cDNA	Hs.77813	X59960	402620	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase) (SMPD1), mRNA /cds=(0,1889)	1	CCCTGTACTGCTGCTGACCTGATG CTGCCAGTCGTAAAATAAGAT
8060	HUVEC cDNA	Hs.172690	X62535	30822	diacylglycerol kinase, alpha (80kD) (DGKA), mRNA /cds=(103,2310)	1	ACACACATACACACACCCCCAAACAC ATACATTGAAAGTCCTCATCTGA
8061	HUVEC cDNA	Hs.272822	X63527	36127	RuvB (E coli homolog)-like 1 (RUVBL1), mRNA /cds=(76,1446)	1	ACCTCCCACCTTGCTGTACATACTG GCCTCTGTGATTACATAGATCAGC
8062	HUVEC cDNA	Hs.119529	X67698	37476	epididymal secretory protein (19.5kD) (HE1), mRNA /cds=(10,465)	1	AACAAACATTAACCTGTGGCCTCTTCT ACACCTGGAAATTACTCTTGA
8063	HUVEC cDNA	Hs.211579	X68264	433891	MUC18 gene exons 1&2 /cds=(26,1966)	1	TCTCTGCTCAATCTGCTTGGCTCC AAGGACCTGGATCTCTGGTAGC
8064	HUVEC cDNA	Hs.75061	X70326	38434	macrophage myristoylated alanine-rich C kinase substrate (MACMARCKS), mRNA /cds=(13,600)	1	TGCTTACTCAAGTTCAACCTCCAG CCTGTGAATCAACTGTCTCTT
8065	HUVEC cDNA	Hs.31314	X72841	297903	retinoblastoma-binding protein 7 (RBBP7), mRNA /cds=(287,1564)	1	AACTTTTACACTTTTCTTCAACAC TTCTTGATTGGCTTGAGAAAT
8066	HUVEC cDNA	Hs.79088	X78659	469884	reticulocalbin 2, EF-hand calcium binding domain (RCN2), mRNA /cds=(66,1019)	1	TGGTGAGTGGATTTCAGACATTG TCCAACCTTTTCAATTGAGTGATT
8067	HUVEC cDNA	Hs.7957	X79448	2326523	adenosine deaminase, RNA-specific (ADAR), transcript variant ADAR-a, mRNA /cds=(187,3867)	1	GAGTGAGGAAGACCCCCAACGATAG ACTCGGGTACTGTGATGATGGCTGC
8068	HUVEC cDNA	Hs.76206	X79981	599833	cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), mRNA /cds=(120,2474)	1	TGGCAAAGCCCCACACTGCAAGG GATTGTAGATAACACTGACTTGT
8069	HUVEC cDNA	Hs.172182	Y00345	35569	poly(A)-binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(502,2403)	1	GGAAAGGAAACTTGAACCTTATGTA CCGAGCAAATGCCAGGTCTAGCAA
8070	HUVEC cDNA	Hs.180414	Y00371	32466	hsc70 gene for 71 kd heat shock cognate protein	1	AGTTAAGATTTCAGAAAGTCGGGG ATTGGAGCTAACGCTGCCACCTGGT
8071	HUVEC cDNA	Hs.75216	Y00815	34266	protein tyrosine phosphatase, receptor type, F (PTPRF), mRNA /cds=(370,6063)	1	TTACCTTGTGGATGCTAGTGTCTG AGTTCACTGTGACACAGTCCTG
8072	HUVEC cDNA	Hs.65114	Y07604	1945761	keratin 18 (KRT18), mRNA /cds=(51,1343)	1	GGGGCTTCACATTATCATAACCTCT CCTCTAAAGGGGAGGCATTAAAAT
8073	HUVEC cDNA	Hs.113503	Y08890	2253155	Homo sapiens mRNA for Ran_GTP binding protein 5 (RanBP5(Importin5) gene) /cds=(236,3529)	1	TTTCCTTGTGCAATTCAAGACTTAAGC ATCGAGTTTACCATCTTCCACT
8074	HUVEC cDNA	Hs.44499	Y09703	4581462	pinin, desmosome associated protein (PNN), mRNA /cds=(30,2261)	1	ACATGTGCAAATAATGTGGCTTAGA CTTGTGTGACTGCTTAAGACTAA
8075	HUVEC cDNA	Hs.8887	Y11307	2791897	cysteine-rich, angiogenic inducer, 61 (CYR61), mRNA /cds=(80,1225)	1	AAATGTAGCTTGGGGAGGGAGGG GAAATGTAATACTGGAATAATTG

Table 8

8076	HUVEC cDNA	Hs.90061	Y12711	6759555	progesterone receptor membrane component 1 (PGRMC1), mRNA /cds=(78,665)	1	ACCCACTGAAAAGTAGTAGTCAGTGTCTTTGATATTGCTCTT
8077	HUVEC cDNA	Hs.101033	Y14391	6562622	Pseudoautosomal GTP-binding protein-like (PGPL), mRNA /cds=(329,1540)	1	GCCTGCTGTGAACCTGCTTCCCTCGGAATGTTCCGTAACAGGACATTAA
8078	HUVEC cDNA	Hs.24322	Y15286	2584788	ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 9kD (ATP6H), mRNA /cds=(62,307)	1	GAAGAGCCATCTCAACAGAACATGCCACCAA
8079	HUVEC cDNA	Hs.291904	Z31696	479156	accessory proteins BAP31/BAP29 (DXS1357E), mRNA /cds=(136,876)	1	AGGAGGGTGGGTGGAACAGGTGGAC
8080	HUVEC cDNA	Hs.180877	Z48950	761715	clone PP781 unknown mRNA /cds=(113,523)	1	TGGAGTTCTCTTGAGGGCAATAAA
8081	HUVEC cDNA	Hs.289101	Z49835	860985	glucose regulated protein, 58kD (GRP58), mRNA /cds=(0,1517)	1	TGCTTGTAAAGATGCCATAATAGTCAGTATTTGCAAGTGGGGGGTGGGGGGTATTCTAATT
8082	HUVEC cDNA	Hs.10340	AK000452	7020548	hypothetical protein FLJ20445 (FLJ20445), mRNA /cds=(334,1170)	1	TTGGGGGAAATGTTGTGGGGGGTGGGGGGTATTCTAATT
8083	HUVEC cDNA	Hs.194676	AK001313	7022490	tumor necrosis factor receptor superfamily, member 6b, decoy (TNFRSF6B), transcript variant 2, mRNA /cds=(827,4486)	1	AGCATGGTAAACCTGGGTTTGTCAACACAGACAGAAATGCAA
8084	HUVEC cDNA	Hs.808	AK001364	7022577	heterogeneous nuclear ribonucleoprotein F (HNRPF), mRNA /cds=(323,1570)	1	GGTCTTGTACTAATCACCAAAAGCAACCAACTTAGCCAGTTTATT
8085	HUVEC cDNA	Hs.15978	AK002211	7023952	cDNA FLJ11349 fis, clone PLACE4000650, weakly similar to TUBERIN /cds=UNKNOWN	1	GCCGATTCCAAGCGAGGGATTTAACCTTACATTGGCCATTGGCTC
8086	HUVEC cDNA	Hs.28692	AK021498	10432693	cDNA FLJ11436 fis, clone HEMBA1001213 /cds=UNKNOWN	1	TTCCCTGGACAGTTGATGTGCTTATGGTGGAGTTATAATCTGCTGT
8087	HUVEC cDNA	Hs.109672	AK023900	10435975	Homo sapiens, Similar to sialytransferase 7 ((alpha-N-acetyleneuraminyl 2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialytransferase) F, clone MGC:14252 IMAGE:4128833, mRNA, complete cds /cds=(128,1129)	1	GGCCGTGACTGCCAGACTGGGTTTGTAATGTTGACAGGAATAAA
8088	HUVEC cDNA	Hs.25635	AK024039	10436304	cDNA FLJ13977 fis, clone Y79AA1001603, weakly similar to POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) /cds=(418,1791)	1	TGACCATTGGAGGGCGGGGCCTCCTAGAAGAACCTCTTAGACAATGG
8089	HUVEC cDNA	Hs.288967	AK024167	10436481	cDNA FLJ14105 fis, clone MAMMA1001202 /cds=UNKNOWN	1	CAGTCCTCACACCAGCCAAGGTCAAGCAAGAGAAACTGA
8090	HUVEC cDNA	Hs.25001	AK024230	10436557	cDNA FLJ14168 fis, clone NT2RP2001440, highly similar to mRNA for 14-3-3gamma /cds=UNKNOWN	1	CCTCAGTGTGAAATATCATGAATGTGAGTCATTATGAGCTGCTAC
8091	HUVEC cDNA	Hs.6101	AK025006	10437439	hypothetical protein MGC3178 (MGC3178), mRNA /cds=(81,1055)	1	ACACACAACTTCAGCTTGCATCACAGTCAGTGTATTCCAAGAAATCAA
8092	HUVEC cDNA	Hs.322680	AK025200	10437664	cDNA: FLJ21547 fis, clone COL06208 /cds=UNKNOWN	1	GGAATTTCGCACCAAGAGGACCCACCAGTCCTCGCTGACATCTGGAAC
8093	HUVEC cDNA	Hs.288061	AK025375	10437878	actin, beta (ACTB), mRNA /cds=(73,1200)	1	GGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCAAGTTGAATAAA
8094	HUVEC cDNA	Hs.288869	AK025842	10438480	nuclear receptor subfamily 2, group F, member 2 (NR2F2), mRNA /cds=(342,1586)	1	CAGAGAAAGAAAAGGCAAAGACTGTTTTGCTTAATTCCCTCTGT
8095	HUVEC cDNA	Hs.251653	AK026594	10439481	tubulin, beta, 2 (TUBB2), mRNA /cds=(0,1337)	1	GAAAGCAGGGAAGCAGTGTGAACCTTTACTCAGCTCCAGCTGTCTGT
8096	HUVEC cDNA	Hs.334842	AK026632	10439528	tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA /cds=(67,1422)	1	TGTTTAGATTGTTTCACTTGGTGTACATGCTTGTACCTGT
8097	HUVEC cDNA	Hs.288036	AK026650	10439548	tRNA isopentenylpyrophosphate transferase (IPT), mRNA /cds=(80,1040)	1	TGCATCGAAACCTTCAGAAGGAAAGGAATGTTGACCACTT
8098	HUVEC cDNA	Hs.324406	AK026741	10439662	ribosomal protein L41 (RPL41), mRNA /cds=(83,160)	1	GGACCTGTGACATTCTGGACTATTCTGTGTTTGTGGCCAGTGT
8099	HUVEC cDNA	Hs.274368	AK026775	10439706	MSTP032 protein (MSTP032), mRNA /cds=(58,319)	1	TGCAACTAGCAACTCATCTTCGGAAGACACAGCCAGGAGAAATGAAGTAGA
8100	HUVEC cDNA	Hs.289071	AK027187	10440255	cDNA: FLJ22245 fis, clone HRC02612 /cds=UNKNOWN	1	GACTTCTCTCTGAGCTTCTACTTCTAAGTCTGAATCCAGTCAGAAA
8101	HUVEC cDNA	Hs.334788	BG385658	13278634	hypothetical protein FLJ14639 (FLJ14639), mRNA /cds=(273,689)	1	GTTCTCTTTGGTTTCCAGATTTCT
8102	HUVEC cDNA	NA	NC_002090	9507429	many cloning vectors, kanamycin resistance, gene	1	TTAGAACCGTGACTGACCCCTCTGAGCAATAACTAGCATAACCCCTT
8103	HUVEC cDNA	NA	U07360	476289	Human DKS1178 locus dinucleotide repeat polymorphism sequence	1	GGGGCCTCTAAACGGGTCTTGAGG
8104	HUVEC cDNA	Hs.230165	AA449779	2163529	zx09e02.s1 cDNA, 3' end /clone=lIMAGE:785978 /clone_end=3'	1	TGCCCATTCACATTGCTCATTACTCA
						1	TGCAAATTCTCTTGCTAACCTACCCAGGAACTTGGTTAAAGTTATGCT
						1	ACCCACCATGGTAAAGATTCAAGGGAACTTGGTTAAAGTTATGCT

Table 8

8105	HUVEC cDNA	NA	AI000459	3191013	ot07c08.s1 NCL_CGAP_GC3 cDNA clone IMAGE:1614158 3' similar to gb:Y00361 60S RIBOSOMAL PROTEIN (HUM)	1	GTCAAATAAGGGTGTCTTCCTTGAA GGACAGCACCCATGCCACAGCAC
8106	HUVEC cDNA	Hs.172922	AI016204	3230540	ot83f03.s1 cDNA, 3' end /clone=IMAGE:1623389 /clone_end=3'	1	CTGGAAAAACATCACATGGTTGAGTC AAGGATGAAAAGTCAAAACCTACCT
8107	HUVEC cDNA	Hs.96457	AI081571	3418363	ox59h10.s1 cDNA, 3' end /clone=IMAGE:1660675 /clone_end=3'	1	ATCCATCCAATAAACACAGCAACACC CTATGCTACTGACCAAGCAAAGCT
8108	HUVEC cDNA	NA	AI082318	3419110	ox72c08.x1 Soares_NhHMPu_S1 cDNA clone IMAGE:1661870 3' similar to gb:X63527 60S RIBOSOMAL PROTEIN	1	TAGTTAGAGTCCAAGACATGGTTCTT CCCCCTTGTCGTACATCCTGGC
8109	HUVEC cDNA	Hs.145222	AI187426	3738064	qf31d08.x1 cDNA, 3' end /clone=IMAGE:1751631 /clone_end=3'	1	CAGCCTGCCTGCTGGCCATTTCCTT CCCCTTCATTTCTAACCTCGA
8110	HUVEC cDNA	Hs.273194	AI285483	3923716	ty56b02.x1 cDNA, 3' end /clone=IMAGE:2283051 /clone_end=3'	1	ACTTCCTCCCCCTCCCCTAGCATTA CTTATATGATATGTTCCATACCC
8111	HUVEC cDNA	Hs.238797	AI307808	4002412	602081661F1 cDNA, 5' end /clone=IMAGE:4245999 /clone_end=5'	1	AAGGAATTGTTTCCCTATCTTAAC TCACTAACAGAGGGTTACTCGA
8112	HUVEC cDNA	Hs.135872	AW028193	5886949	wv61h08.x1 cDNA, 3' end /clone=IMAGE:2534079 /clone_end=3'	1	TTTGCATCCCGAGTTTGTATTCCAA GAAAATCAAAGGGGGCCAATTGT
8113	HUVEC cDNA	Hs.244816	AW078847	6033999	xb18g07.x1 cDNA, 3' end /clone=IMAGE:2576700 /clone_end=3'	1	AAACAGGAAGGGGGTTGGGCCCTT TGATCAACTGGAACCTTGGATCAAG
8114	HUVEC cDNA	Hs.249883	AW162315	6301348	au66d07.x1 cDNA, 3' end /clone=IMAGE:2781229 /clone_end=3'	1	AAAAACGGTTATGGGGTAGGGAAA CAGGCGAAAAGAACGTGGAGAAA
8115	HUVEC cDNA	Hs.329930	AW170757	6402282	xj24e07.x1 cDNA, 3' end /clone=IMAGE:2658180 /clone_end=3'	1	GGGGACTCAGGCCCGCTGGGGT CCCACATAGGGTTTATCCAAAAAA
8116	HUVEC cDNA	Hs.23349	AW237511	6569800	nab70è03.x1 cDNA, 3' end /clone=IMAGE:3273292 /clone_end=3'	1	TGTTGTTGGATACGTACTTAACGGT ATGCATCCCATGCTTTGGGTACT
8117	HUVEC cDNA	NA	BE672733	10033274	7b75g07.x1 NCL_CGAP_Lu24 cDNA clone IMAGE:3234108 3' similar to TR:O99231 O99231 CYTOCHROME OXIDASE	1	TGAGAGCACACCATAAATTACAGCA GGAATAAACGAAACACAGCAGCA
8118	HUVEC cDNA	Hs.288443	BF110312	10940002	7n36d08.x1 cDNA, 3' end /clone=IMAGE:3566654 /clone_end=3'	1	ACCAAGGGCTAAACCTCAATTATG TTCACTGACAGTGGGATTTCTT
8119	HUVEC cDNA	Hs.111301	J03210	180670	matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase) (MMP2), mRNA /cds=(289,2271)	1	AGCCATAGAAGGTGTCAGGTATTGC ACTGCCAACTCTTGTCGTTT
8120	HUVEC cDNA	Hs.82085	M14083	189566	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 (SERPINE1), mRNA /cds=(75,1283)	1	CCATGCCCTTGTATCAATCTGAAT CCCATAGCTGCTTGAATCTGCTGC
8121	HUVEC cDNA	Hs.80120	Y10343	2292903	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1), mRNA /cds=(31,1710)	1	TTAAGAATGTGGCAGAAATGTATGCT GAGGTAGCCCAGTCAATCCTTATT
8122	HUVEC cDNA	Hs.10340	AK000452	7020548	hypothetical protein FLJ20445 (FLJ20445), mRNA /cds=(334,1170)	1	ATCAGTAGCAAAACAAACCCAGCAAC TTCTGTCAGCATCTGCTGTAGGG
8123	HUVEC cDNA	Hs.73742	AK001313	7022490	cDNA FLJ10451 fis, clone NT2RP1000959, highly similar to acidic ribosomal phosphoprotein P0 mRNA /cds=UNKNOWN	1	CCCATCTAACTAGCACACGAACCTTC CACGAGGACGCTGGCAGAGAAG
8124	HUVEC cDNA	Hs.808	AK001364	7022577	heterogeneous nuclear ribonucleoprotein F (HNRPF), mRNA /cds=(323,1570)	1	GAACCTGGCAGTTGTAGCAGAGGCCA GTTGAGGCTTGTGACCATCACCAT
8125	HUVEC cDNA	Hs.15978	AK002211	7023952	cDNA FLJ11349 fis, clone PLACE4000650, weakly similar to TUBERIN /cds=UNKNOWN	1	CGCTCTCCTGCACAGCACACACAC CAACAGTCTGGATGATTTAGGCA
8126	HUVEC cDNA	Hs.29692	AK021498	10432693	cDNA FLJ11438 fis, clone HEMBA1001213 /cds=UNKNOWN	1	TTTTGGGAAGAAACCCATGCTATGCT GAAATACAATTGGCAATGGAAAGCT
8127	HUVEC cDNA	Hs.109672	AK023900	10435975	Homo sapiens, Similar to sialytransferase 7 ((alpha-N-acetylneuraminy 2,3-beta galactosyl-1,3)-N-acetyl galactosamidase alpha-2,6-sialytransferase) F, clone MGC:14252 IMAGE:4128833, mRNA, complete cds /cds=(128,1129)	1	CTCTTGTGCTACTCATTTCTCCG GCGCTGCTGAGGGTAGGTGTC

Table 8

8128	HUVEC cDNA	Hs.25635	AK024039	10436304	cDNA FLJ13977 fis, clone Y79AA1001603, weakly similar to POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41) /cds=(418,1791)	1	CAACTTCCCTTGGTTACCCAGAAGA ACAGCAGCACCGTGATCCAGAGCA
8129	HUVEC cDNA	Hs.288967	AK024167	10436481	cDNA FLJ14105 fis, clone MAMMA1001202 /cds=UNKNOWN	1	CTGTACATCTGCATCCCAGCAAAGAG CAGCAGGGACAGGAGGGAGGAGAG
8130	HUVEC cDNA	Hs.25001	AK024230	10436557	cDNA FLJ14168 fis, clone NT2RP2001440, highly similar to mRNA for 14-3-3gamma /cds=UNKNOWN	1	CACAGACAGAAGGTTTCGTTCTCAT TCGACAGTGGCTATTCTAGCTCTG
8131	HUVEC cDNA	Hs.6101	AK025006	10437439	hypothetical protein MGC3178 (MGC3178), mRNA /cds=(81,1055)	1	TCAAGATTGGCAATTCACTGTGCCCA TAAACCACACTCAGTAGCTCAGCCT
8132	HUVEC cDNA	Hs.322680	AK025200	10437684	cDNA: FLJ21547 fis, clone COL06206 /cds=UNKNOWN	1	AGTTGTCCTGAGAGTTTACACTTGT GAGAAAATACTGGCAGCTTGATT
8133	HUVEC cDNA	Hs.288061	AK025375	10437878	actin, beta (ACTB), mRNA /cds=(73,1200)	1	CACATAGGAATCCTCTGACCCATGC CCACCATCACGCCCTGGTGCTGG
8134	HUVEC cDNA	Hs.288869	AK025842	10438480	nuclear receptor subfamily 2, group F, member 2 (NR2F2), mRNA /cds=(342,1586)	1	AACAGGAACCTTATCTCTTTGTGAG GCGATTTGCATTCTCACACAGGC
8135	HUVEC cDNA	Hs.251653	AK026594	10439481	tubulin, beta, 2 (TUBB2), mRNA /cds=(0,1337)	1	GTAATTGCCGCCGGTGGCCTCATTGT AGTACACGTTGATGCGTCCAGCT
8136	HUVEC cDNA	Hs.278242	AK026632	10439528	Homo sapiens, clone MGC:3214 IMAGE:3502620, mRNA, complete cds /cds=(2066,3421)	1	ATAGTGGCTAGGGATTAGGAGGCAG AGGCAGACAGGAGCAGACACGGGTC
8137	HUVEC cDNA	Hs.181165	AK026650	10439548	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(53,1441)	1	CATTTGGCTTTAGGGTAGTTTC ACGACACCTGTGTTCTGGCGGCAA
8138	HUVEC cDNA	Hs.108124	AK026741	10439662	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	1	CCCTGGTTCAGGAATTAAGGGGACA GACTTGAAATAAGGAAACAAAACAAA
8139	HUVEC cDNA	Hs.274368	AK026775	10439706	MSTP032 protein (MSTP032), mRNA /cds=(68,319)	1	ACAGTAGAGAAATTGAGTACACAGGG TATGGAGAGTAGGGCACAAAATGT
8140	HUVEC cDNA	Hs.241507	AK027187	10440255	cDNA: FLJ23534 fis, clone LNG06974, highly similar to HUMRPS6A ribosomal protein S6 mRNA /cds=UNKNOWN	1	GAACAGCCTCGTCTTCCCCGAATGC CAGGCAGGATGACGATGAACGTGG
8141	HUVEC cDNA	Hs.334788	BG392671	13286119	hypothetical protein FLJ14639 (FLJ14639), mRNA /cds=(273,689)	1	GACCTCCAGAATTTCCTCATCGCTGT CGGTGACCAAGTCCACAGACACTA
8142	HUVEC cDNA	NA	NC_002090	9507429	many cloning vectors, kanamycin resistance, gene	1	TCTTGCCATCCTATGGAACTGCCCTCG TGAGTTTCTCTTCAATTACAGA
8143	HUVEC cDNA	NA	U07360	476289	Human DDX178 locus dinucleotide repeat polymorphism sequence	1	TGTTACTCCTCAAGCCCCCTGAATCA CTATAGGCCACGACTCTCCAACCTGA

TABLE 9: Cardiac Transplant patient RNA samples and array hybridizations

Patient #	Sample	Rejection Grade	RNA Yield (µg)	Hybridization #
14-0001	1			
	2	3A	13.6	107739
	3	1A	5.83	107740
14-0002	1			
	2			
	3			
14-0003	1	0	12.8	
	2			
	3			
14-0004	1			
	2			
14-0005	1	3A	1.08	107741
	2	0	11.2	107742
	3			
	4			
14-0006	1	2	2.02	
	2			
	3			

TABLE 10: Differentially expressed probes between samples from patients with high and low grade rejection:

Oligo#	Gene Represented
7401	cDNA clone IMAGE:915561
1796	amphiregulin
4423	partial IGVH3 gene for immunoglobulin heavy chain V region
4429	partial IGVL1 gene for immunoglobulin lambda light chain V region
4430	partial IGVH3 DP29 gene for immunoglobulin heavy chain V region
4767	cDNA clone COL09252, highly similar to CD24
4829	oncostatin M
8091	mRNA for a predicted protein

We claim:

1. A system for detecting gene expression comprising at least two isolated DNA molecules wherein each isolated DNA molecule detects expression of a gene wherein said gene is selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO:1 - SEQ ID NO: 8143.
2. The system of claim 1 wherein said gene is selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO:2476, SEQ ID NO: 2407, SEQ ID NO:2192, SEQ ID NO: 2283, SEQ ID NO:6025, SEQ ID NO: 4481, SEQ ID NO:3761, SEQ ID NO: 3791, SEQ ID NO:4476, SEQ ID NO: 4398, SEQ ID NO:7401, SEQ ID NO: 1796, SEQ ID NO:4423, SEQ ID NO: 4429, SEQ ID NO:4430, SEQ ID NO: 4767, SEQ ID NO:4829, and SEQ ID NO: 8091.
3. The system of claim 1 wherein the DNA molecules are synthetic DNA, genomic DNA, PNA or cDNA.
4. The system of claim 1 wherein the isolated DNA molecules are immobilized on an array.
5. The system of claim 4 wherein the array is selected from the group consisting of a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, polynucleotide array or a cDNA array, a microtiter plate, a membrane and a chip.
6. A method of detecting gene expression comprising a) isolating RNA and b) hybridizing said RNA to the isolated DNA molecules of claim 1.
7. A method of detecting gene expression comprising a) isolating RNA; b) converting said RNA to nucleic acid derived from the RNA and c) hybridizing said nucleic acid derived from the RNA to the isolated DNA molecules of claim 1.
8. The method of claim 7 wherein said nucleic acid derived from the RNA is cDNA.

9. A method of detecting gene expression comprising a) isolating RNA; b) converting said RNA to cRNA or aRNA and c) hybridizing said cRNA or aRNA to the isolated DNA molecules of claim 1.
10. A candidate library comprising at least two isolated oligonucleotides wherein the oligonucleotides have nucleotide sequences having at least 40-50, 50-60, 70-80, 80-85, 85-90, 90-95 or 95-100% sequence identity to the nucleotide sequences selected from the group consisting of SEQ ID NO:1- SEQ ID NO: 8143.
11. The candidate library of claim 10, wherein the nucleotide sequence comprises deoxyribonucleic acid (DNA) sequence, ribonucleic acid (RNA) sequence, synthetic oligonucleotide sequence, protein nucleic acid (PNA) sequence or genomic DNA sequence.
12. The candidate library of claim 11, wherein the candidate library is immobilized on an array.
13. The candidate library of claim 12, wherein the array is selected from the group consisting of: a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, polynucleotide array or a cDNA array, a microtiter plate, a membrane and a chip.
14. A diagnostic oligonucleotide for a disease comprising an oligonucleotide wherein the oligonucleotide has a nucleotide sequence selected from the group consisting of SEQ ID NO:1 - SEQ ID NO: 8143 wherein said oligonucleotide detects expression of a gene that is differentially expressed in leukocytes in an individual with at least one disease criterion for at least one leukocyte-related disease compared to the expression of said gene in an individual without the at least one disease criterion, wherein expression of the gene is correlated with the at least one disease criterion.
15. The diagnostic oligonucleotide of claim 14, wherein the nucleotide sequence comprises DNA, cDNA, PNA, genomic DNA, or synthetic oligonucleotides.

16. The diagnostic oligonucleotide of claim 14, wherein the disease criterion comprises data wherein the data is selected from physical examination data, laboratory data, patient historic, diagnostic, prognostic, risk prediction, therapeutic progress, and therapeutic outcome data.
17. The diagnostic oligonucleotide of claim 14, wherein the leukocytes comprise peripheral blood leukocytes or leukocytes derived from a non-blood fluid.
18. The diagnostic oligonucleotide of claim 17, wherein the non-blood fluid is isolated from the colon, sinus, esophagus, small bowel, pancreatic duct, biliary tree, ureter, vagina, cervix uterus, nose, ear, urethra, eye, open wound, abscess, stomach, cerebral spinal fluid, peritoneal fluid, pleural fluid, synovial fluid, bone marrow and pulmonary lavage.
19. The diagnostic oligonucleotide of claim 14, wherein the leukocytes comprise leukocytes derived from urine or a biopsy sample.
20. The diagnostic oligonucleotide of claim 14, wherein the leukocytes are peripheral blood mononuclear cells or T-lymphocytes.
21. The diagnostic oligonucleotide of claim 14, wherein the disease is selected from the group consisting of cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus (SLE), rheumatoid arthritis, osteoarthritis, and cytomegalovirus infection.
22. The diagnostic oligonucleotide of claim 14, wherein the differential expression is one or more of: a relative increase in expression, a relative decrease in expression, presence of expression or absence of expression.
23. A diagnostic agent comprising an oligonucleotide wherein the oligonucleotide has a nucleotide sequence selected from the group consisting of SEQ ID NO:1 - SEQ ID NO: 8143 wherein said oligonucleotide detects expression of a gene that is differentially expressed in leukocytes in an individual over time.

24. The agent of claim 23 wherein said oligonucleotide is selected from the group consisting of SEQ ID NO:2476, SEQ ID NO: 2407, SEQ ID NO:2192, SEQ ID NO:2283, SEQ ID NO:6025, SEQ ID NO:4481, SEQ ID NO:3761, SEQ ID NO:3791, SEQ ID NO:4476, SEQ ID NO:4398, SEQ ID NO:7401, SEQ ID NO: 1796, SEQ ID NO:4423, SEQ ID NO:4429, SEQ ID NO:4430, SEQ ID NO:4767, SEQ ID NO:4829, and SEQ ID NO:8091.
25. A diagnostic probe set for a disease comprising at least two probes wherein each probe detects expression of a gene wherein the gene is selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO: 1 - SEQ ID NO:8143 wherein each gene is differentially expressed in leukocytes in an individual with at least one disease criterion for a disease selected from Table 1 as compared to the expression of the gene in leukocytes in an individual without the at least one disease criterion, wherein expression of the gene is correlated with the at least one disease criterion.
26. An isolated nucleic acid wherein said nucleic acid comprises a sequence depicted in SEQ ID NO:8144 - SEQ ID NO:8766.
27. An expression vector containing the nucleic acid of claim 26 in operative association with a regulatory element which controls expression of the nucleic acid in a host cell.
28. A host cell comprising the expression vector of claim 27.
29. The host cell of claim 27, wherein the host cell is a prokaryotic cell or a eukaryotic cell.
30. A kit comprising the system of claim 1.
31. A system for detecting gene expression in leukocytes comprising an isolated DNA molecule wherein said isolated DNA molecule detects expression of a gene wherein said gene is selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO: 1-SEQ ID NO: 8143 and said gene is differentially expressed in said leukocytes in an individual with at least one disease

criterion for a disease selected from Table 1 compared to the expression of said gene in leukocytes in an individual without the at least one disease criterion.

32. The system of claim 31 wherein the DNA molecule is at least 16 nucleotides in length.

33. The system of claim 31 wherein the DNA molecules are synthetic DNA, genomic DNA, PNA or cDNA.

34. The system of claim 31 wherein the isolated DNA molecule is immobilized on an array.

35. The system of claim 34 wherein the array is selected from the group consisting of a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, polynucleotide array or a cDNA array, a microtiter plate, a membrane and a chip.

36. A method of detecting gene expression comprising a) isolating RNA and b) hybridizing said RNA to the isolated DNA molecule of claim 31.

37. A method of detecting gene expression comprising a) isolating RNA; b) converting said RNA to nucleic acid derived from the RNA and c) hybridizing said nucleic acid derived from said RNA to the isolated DNA molecules of claim 31.

38. The method of claim 37 wherein said nucleic acid derived from the RNA is cDNA.

39. A method of detecting gene expression comprising a) isolating RNA; b) converting said RNA to cRNA or aRNA and c) hybridizing said cRNA or aRNA to the isolated DNA molecule of claim 31.

40. A method of diagnosing a disease comprising obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31 and comparing the expression of the gene with a molecular signature indicative of the presence or absence of said disease.

41. A method of monitoring progression of a disease comprising: obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of disease progression.

42. A method of monitoring the rate of progression of a disease comprising: obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of disease progression.

43. A method of predicting therapeutic outcome comprising: obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the predicted therapeutic outcome.

44. A method of determining prognosis for a patient comprising obtaining a leukocyte sample from a patient, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene, and comparing the expression of the gene with a molecular signature indicative of the prognosis.

45. A method of predicting disease complications in an individual comprising obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of disease complications.

46. A method of monitoring response to treatment in an individual, comprising obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of response to treatment.

47. The method according to claim 46, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.
48. The method according to claim 41, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.
49. The method according to claim 42, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.
50. The method according to claim 43, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.
51. The method according to claim 44, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.
52. The method of claim 50, wherein the genotype is analyzed by one or more methods selected from the group consisting of Southern analysis, RFLP analysis, PCR, single stranded conformation polymorphism, and SNP analysis.
53. A method of RNA preparation suitable for diagnostic expression profiling comprising: obtaining a leukocyte sample from a subject, adding actinomycin-D to a final concentration of 1 ug/ml, adding cycloheximide to a final concentration of 10 ug/ml, and extracting RNA from the leukocyte sample.
54. The method of claim 52, wherein the actinomycin-D and cycloheximide are present in a sample tube to which the leukocyte sample is added.

Figure 1: Novel Gene Sequence Analysis

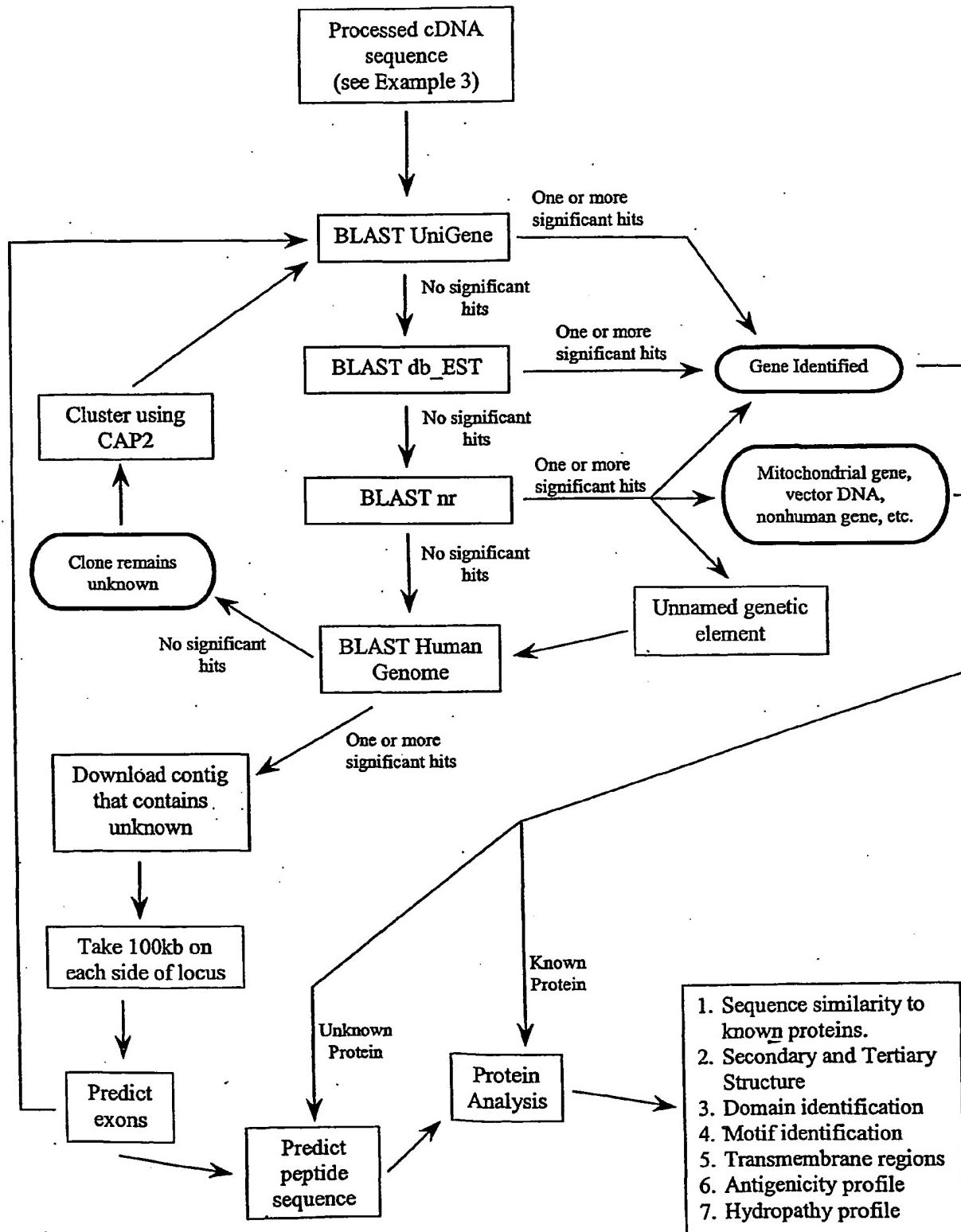


Figure 2 . Automated Mononuclear Cell RNA Isolation Device

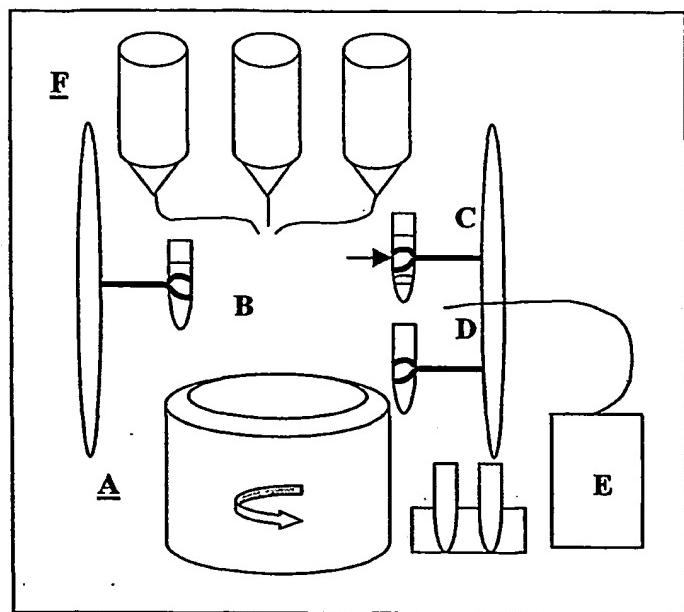


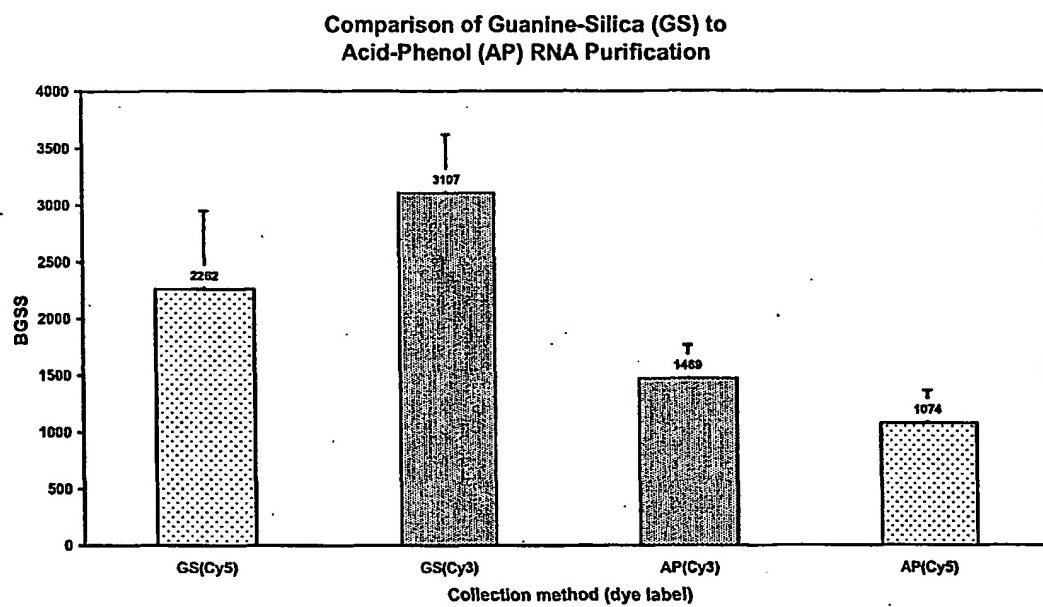
Figure 3: Kits for discovery, or application of diagnostic gene sets**A. Contents of kit for discovery of diagnostic gene sets**

1. Sterile, endotoxin and RNase free blood collection tubes (>10cc capacity)
2. Alcohol swabs, tourniquet, 18g needle and syringe (>10cc capacity)
3. Erythrocyte lysis buffer
4. Leukocyte lysis buffer
5. Substrates for labeling of RNA (may vary for various expression profiling techniques)
 - For fluorescence cDNA microarray expression profiling:
 - Reverse transcriptase and 10x RT buffer
 - Poly-dT primer
 - DTT
 - Deoxynucleotides 100mM each
 - RNAse inhibitor
 - Cy3 and Cy5 labeled deoxynucleotides
6. cDNA microarrays containing candidate gene libraries
7. Cover slips for slides
8. hybridization chambers
9. Software package for identification of diagnostic gene set from data
 - Contains statistical methods.
 - Allows alteration in desired sensitivity and specificity of gene set.
 - Software facilitates access to and data analysis by centrally located database server.
10. Password and account number to access central database server.
11. Kit User Manual

B. Contents of kit for application of diagnostic gene sets

1. Sterile, endotoxin and RNase free blood collection tubes (>10cc capacity)
2. Alcohol swabs, tourniquet, 18g needle and syringe (>10cc capacity)
3. Erythrocyte lysis buffer
4. Leukocyte lysis buffer
5. Substrates for labeling of RNA (may vary for various expression profiling techniques)
 - For fluorescence cDNA microarray expression profiling:
 - Reverse transcriptase and 10x RT buffer
 - Poly-dT primer
 - DTT
 - Deoxynucleotides 100mM each
 - RNAse inhibitor
 - Cy3 and Cy5 labeled deoxynucleotides
6. cDNA microarrays containing diagnostic gene sets
7. cover slips for slides
8. hybridization chambers
9. Software package for identification of diagnostic gene set from data
 - Contains statistical methods.
 - Allows alteration in desired sensitivity and specificity of gene set.
 - Software facilitates access to and data analysis by centrally located database server
10. Password and account number to access central database server.
11. Kit User Manual

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Figure 4

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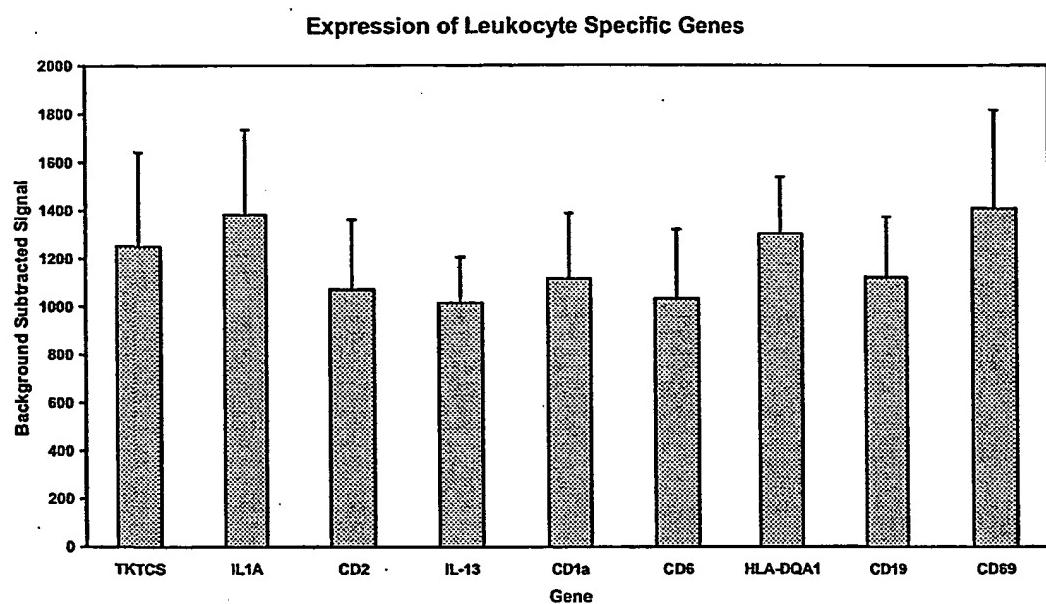
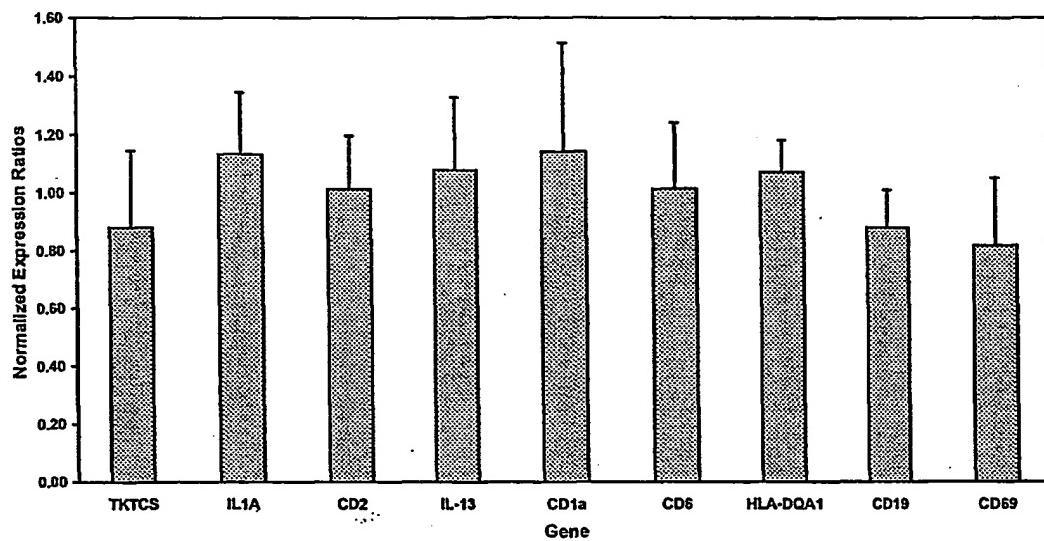
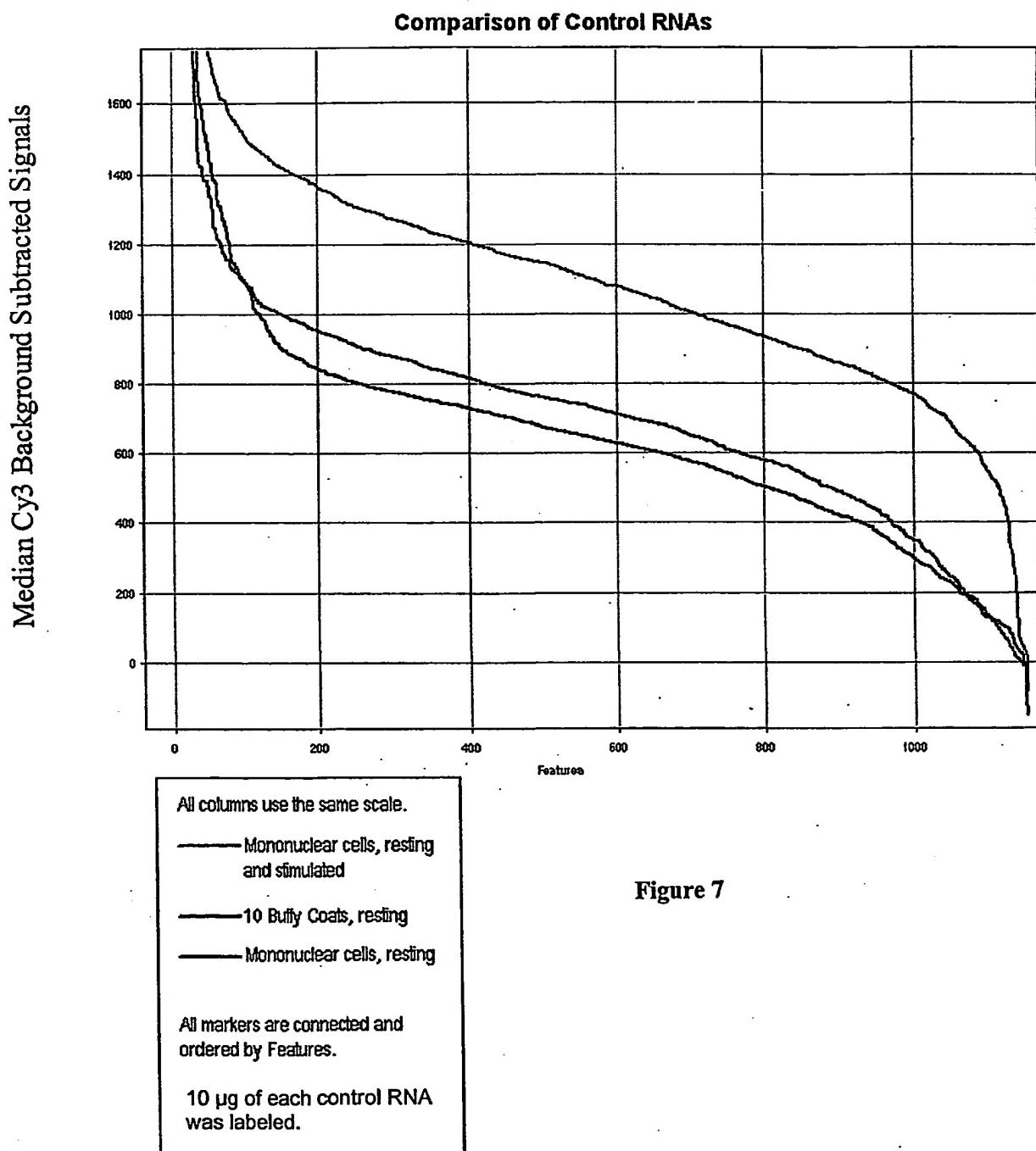


Figure 5

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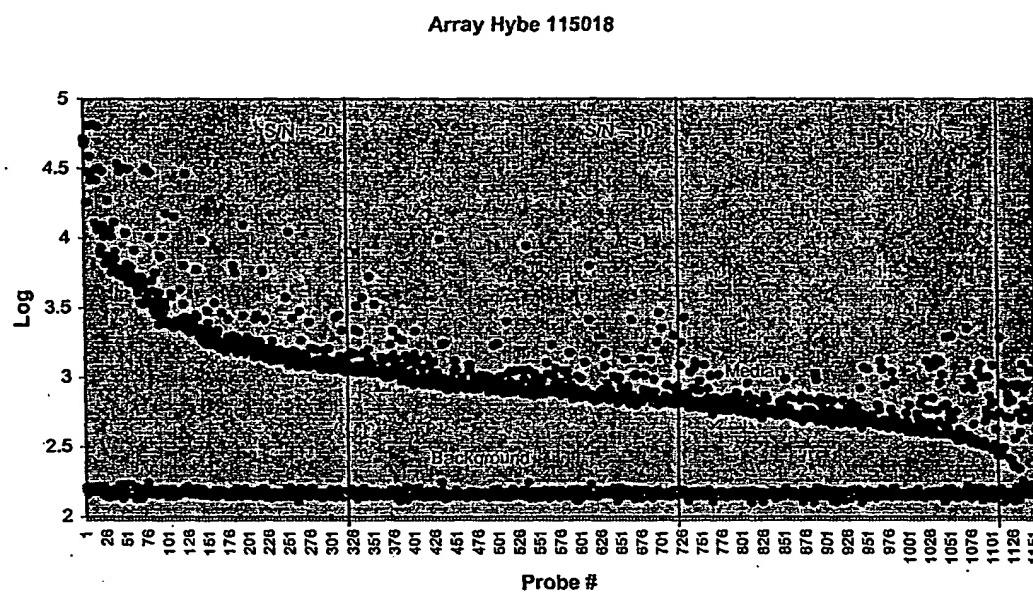
Figure 6**Expression of Leukocyte-Specific Genes**

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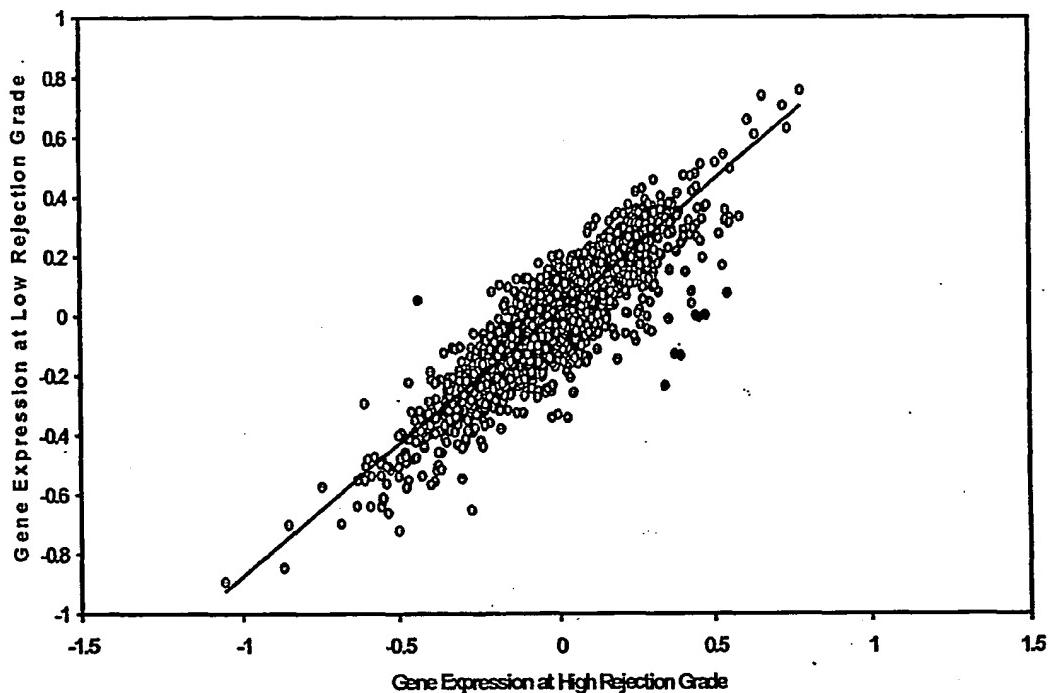
**Figure 7**

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Figure 8: Log expression of each probe using the R50 reference RNA. Probe expression is ordered by Signal to noise, S/N, decreasing from left to right.



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Figure 9**Comparison of High Rejection Grade to Low Rejection Grade**

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Figure 10: Differential gene expression between grade 0 and 3A samples:

Acc #	Name	Gene ID	Array 107742: Grade 0				Array 107739: Grade 3A				Ratio of SRs	
			F633. Median - B632	F532. Median - B532	SR: scaled ratio (a/r)	F633. Median - B632	F532. Median - B532	SR: scaled ratio (a/r)	Grade 0/3A	Grade 3A/0		
NM_003202	transcription factor 7 (T-cell specific, HMG-box) (TCF7)	2476	5558	1050	0.188917	0.710038	5927	358	0.061438	0.219793	3.23048873	0.30955069
BE220959	major histocompatibility complex, class II, DQ beta 1 (HLA-DQ beta 1)	6025	1810	635	0.350828	1.318579	2150	252	0.117209	0.419312	3.14462275	0.31800317
BE220959	major histocompatibility complex, class II, DQ beta 1 (HLA-DQ beta 1)	6025	1402	487	0.347361	1.305545	2121	247	0.116455	0.416612	3.13371958	0.31910959
NM_002922	regulator of G-protein signalling 1 (RGS1), mRNA /cds=	2407	804	95	0.118169	0.444098	1884	75	0.035809	0.142415	3.11833431	0.32058403
NM_001781	CD69 antigen (p60, early T-cell activation antigen) (CD6)	2192	4121	405	0.098277	0.369371	7385	254	0.034394	0.123043	3.00195843	0.33311587
NM_002341	lymphotoxin beta (TNF superfamily, member 3) (LTB), tr	2283	13488	3447	0.25556	0.960516	29882	2727	0.091259	0.326476	2.94207495	0.33989617
BE220959	major histocompatibility complex, class II, DQ beta 1 (HLA-DQ beta 1)	6025	1539	515	0.334533	1.257707	1942	237	0.122039	0.436591	2.88074602	0.3471323
NM_001781	CD69 antigen (p60, early T-cell activation antigen) (CD6)	2192	3850	398	0.10028	0.376823	7705	282	0.0368	0.130934	2.87796558	0.34746767
UD5040	far upstream element (FUSE) binding protein 1 (FUBP1)	3581	4507	1119	0.24828	0.933154	2390	220	0.09205	0.329308	2.83368583	0.35259603
X14008	nuclear receptor subfamily 4, group A, member 2 (NR4A)	3729	1365	167	0.122344	0.459827	6541	434	0.045488	0.162731	2.82568319	0.35589672
NM_003202	transcription factor 7 (T-cell specific, HMG-box) (TCF7)	2476	2718	486	0.17894	0.672539	5310	358	0.067043	0.233845	2.80405488	0.3565264
AF035947	cytokine-inducible inhibitor of signalling type 1b mRNA	642	9850	5254	0.533404	2.004771	969	197	0.203302	0.727307	2.75642938	0.36278818
NM_001781	CD69 antigen (p60, early T-cell activation antigen) (CD6)	2192	3357	356	0.106047	0.398574	5963	246	0.041254	0.147586	2.70062225	0.37028503
Y14737	mRNA for immunoglobulin lambda heavy chain /cds=(65	4905	1390	248	0.178417	0.670576	6561	5767	0.87892	3.444527	0.21325167	4.68929496
Y14737	mRNA for immunoglobulin lambda heavy chain /cds=(65	4905	1398	240	0.171674	0.645231	7159	6112	0.853751	3.054262	0.21125576	4.73359803
BC006402	mRNA for immunoglobulin lambda heavy chain /cds=(65	4481	1826	295	0.161555	0.6072	2973	2498	0.840229	3.005889	0.20200364	4.95040578
X57812	rearranged immunoglobulin lambda light chain mRNA /c	3761	6512	747	0.114711	0.431139	27381	17730	0.647529	2.316519	0.18611538	5.37301111
X57812	rearranged immunoglobulin lambda light chain mRNA /c	3761	6728	755	0.112218	0.421766	28280	18638	0.646634	2.313311	0.18232143	5.48481857
X72475	cDNA: RFL21321 fs, clone COL02335, highly similar to	3790	6572	1188	0.138591	0.520689	17322	13892	0.801986	2.669076	0.16155283	5.50803666
X72475	cDNA: RFL21321 fs, clone COL02335, highly similar to	3790	15538	2128	0.136955	0.514739	17637	14245	0.807677	2.889436	0.17814525	5.61339589
X72475	cDNA: RFL21321 fs, clone COL02335, highly similar to	3791	11974	1550	0.130115	0.469034	24281	18781	0.773299	2.768449	0.17677319	5.65896846
X57812	rearranged immunoglobulin lambda light chain mRNA /c	3761	6953	778	0.111894	0.420551	27621	18560	0.671952	2.403886	0.1749461	5.71604812
X72475	cDNA: RFL21321 fs, clone COL02335, highly similar to	3791	10805	1411	0.130588	0.49081	17533	14334	0.817944	2.8247735	0.16781337	5.95900079
X72475	cDNA: RFL21321 fs, clone COL02335, highly similar to	3790	11246	1453	0.129201	0.4856	17074	13863	0.811036	2.904673	0.16717875	5.9816215
AF067420	SNC73 protein (SNC73) mRNA, complete cds /cds=(39	4399	2654	243	0.09156	0.344125	37518	21610	0.57599	2.060585	0.16700357	5.88789503
X72475	cDNA: RFL21321 fs, clone COL02335, highly similar to	3791	10909	1370	0.125584	0.472005	21688	18561	0.856609	3.064488	0.15402406	6.4924922
AF067420	SNC73 protein (SNC73) mRNA, complete cds /cds=(39	4399	1959	181	0.092394	0.34726	30274	19369	0.633979	2.288826	0.15171979	6.59109804
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BC002963	rearranged immunoglobulin mRNA for mu heavy chain e	4474	7538	684	0.09074	0.341044	6038	4037	0.685899	2.391889	0.14258368	7.01342553
BC002963	rearranged immunoglobulin mRNA for mu heavy chain e	4474	8662	780	0.090048	0.338444	4339	2976	0.685642	2.45286	0.13797951	7.24745312
BC002963	rearranged immunoglobulin mRNA for mu heavy chain e	4474	7183	608	0.084644	0.318133	5521	3905	0.708024	2.532831	0.12558874	7.98186351
BC002963	rearranged immunoglobulin mRNA for mu heavy chain e	4475	8986	851	0.094703	0.355938	1587	1275	0.803403	2.874145	0.12384126	9.0746531
BC002963	rearranged immunoglobulin mRNA for mu heavy chain e	4476	11118	1023	0.092013	0.345828	871	682	0.783008	2.801184	0.12345771	8.09963947
BC002963	rearranged immunoglobulin mRNA for mu heavy chain e	4475	7428	730	0.098277	0.36937	1049	890	0.846427	3.035218	0.12169477	8.21727973
BC002963	rearranged immunoglobulin mRNA for mu heavy chain e	4476	10413	933	0.0896	0.336757	625	486	0.7776	2.781857	0.12105563	8.2606647
BC002963	rearranged immunoglobulin mRNA for mu heavy chain e	4475	5841	484	0.082863	0.311436	1694	1344	0.793388	2.838319	0.10972558	9.11394747
AF067420	SNC73 protein (SNC73) mRNA, complete cds /cds=(39	4398	7950	645	0.08103	0.304549	22995	18594	0.813313	2.909559	0.10467052	9.55376803
AF067420	SNC73 protein (SNC73) mRNA, complete cds /cds=(39	4398	11959	992	0.08285	0.311765	14170	12597	0.889891	3.180333	0.0980291	10.2010527
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